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OM nucleic - nucleic search, using sw model

Run on: November 13, 2004, 07:54:49 ; Search time 122 Seconds  
(without alignments)  
11326.013 Million cell updates/sec

Title: US-10-069-304-1

Perfect score: 1944  
Sequence: 1 atgtcttcggcgctctcc.....atagtgcacctctctta 1944

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA:\*

- 1: /cgn2\_6/prodata/1/ina/5A.COMB.seq:\*
- 2: /cgn2\_6/prodata/1/ina/5B.COMB.seq:\*
- 3: /cgn2\_6/prodata/1/ina/6A.COMB.seq:\*
- 4: /cgn2\_6/prodata/1/ina/6B.COMB.seq:\*
- 5: /cgn2\_6/prodata/1/ina/PCITUS.COMB.seq:\*
- 6: /cgn2\_6/prodata/1/ina/backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	192.8	9.9	1593	4	US-09-602-472A-1
2	192.4	9.9	3108	4	US-10-101-464A-886
3	182	9.4	2868	3	US-09-228-986-4
4	182	9.4	2868	4	US-10-101-464A-4
5	179.8	9.2	1488	4	US-09-579-182-4
6	178.4	9.2	3239	3	US-09-228-986-9
7	178.4	9.2	3239	4	US-10-101-464A-9
8	176.4	9.1	1559	4	US-09-602-472A-3
9	174.6	9.0	2432	3	US-09-228-986-7
10	174.6	9.0	2432	4	US-10-101-464A-7
11	173	8.9	1457	4	US-10-101-464A-159
12	168.2	8.7	2175	4	US-10-101-464A-461
13	166.4	8.6	2749	1	US-08-265-628-1
14	162.4	8.4	4104	3	US-08-881-706-1
15	162.4	8.4	4104	4	US-09-823-394-1
16	162.2	8.3	2315	4	US-10-101-464A-874
17	160.2	8.2	4356	4	US-10-101-464A-888
18	159	8.2	758	4	US-10-101-464A-414
19	153.2	7.9	3257	4	US-10-101-464A-455
20	153.2	7.9	3257	4	US-10-101-464A-456
21	153.2	7.9	3715	4	US-10-101-464A-887
22	150.4	7.7	536	4	US-10-101-464A-355
23	149.8	7.6	493	4	US-10-101-464A-243
24	147.4	7.6	551	4	US-10-101-464A-305
25	146.8	7.6	2884	4	US-10-101-464A-291
26	146.8	7.6	3600	4	US-10-101-464A-458
27	146.6	7.5	2571	1	US-07-717-331F-9

28	146.6	7.5	2693	4	US-10-101-464A-873	Sequence 873, App
29	146.6	7.5	2833	1	US-07-717-331F-1	Sequence 1, Appl1
30	144.2	7.4	3222	4	US-10-101-464A-839	Sequence 839, App
31	140.6	7.2	1554	2	US-08-587-680A-24	Sequence 24, Appl
32	139.8	7.2	2114	4	US-09-602-472A-5	Sequence 5, Appl1
33	139.8	7.2	2749	1	US-07-717-331F-4	Sequence 4, Appl1
34	138.2	7.1	2389	3	US-09-228-986-1	Sequence 1, Appl1
35	138.2	7.1	2389	4	US-10-101-464A-1	Sequence 1, Appl1
36	137.4	7.1	771	4	US-10-101-464A-192	Sequence 192, App
37	136.6	7.0	383	4	US-10-101-464A-393	Sequence 393, App
38	135.6	7.0	3237	4	US-10-101-464A-858	Sequence 858, App
39	132.4	6.8	741	4	US-10-101-464A-385	Sequence 385, App
40	132	6.8	3361	4	US-10-101-464A-947	Sequence 947, App
41	131.8	6.8	2728	4	US-10-101-464A-862	Sequence 862, App
42	130.8	6.7	2336	3	US-09-228-986-10	Sequence 10, Appl
43	130.8	6.7	2336	4	US-10-101-464A-10	Sequence 10, Appl
44	130.6	6.7	564	4	US-10-101-464A-359	Sequence 359, App
45	130.6	6.7	567	4	US-10-101-464A-189	Sequence 189, App

#### ALIGNMENTS

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RESULT 1
US-09-602-472A-1
; Sequence 1, Application US/09602472A
; Patent No. 6608240
; GENERAL INFORMATION:
; APPLICANT: Bidney, Dennis L.
; APPLICANT: Hu, Xu
; APPLICANT: Li, Guihua
; TITLE OF INVENTION: Sunflower Disease Resistance Genes
; FILE REFERENCE: 35718/200630
; CURRENT APPLICATION NUMBER: US/09/602,472A
; CURRENT FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/140,876
; PRIOR FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1593
; TYPE: DNA
; ORGANISM: Helianthus annuus
; FEATURE:
US-09-602-472A-1

Query Match          9.9%; Score 192.8; DB 4; Length 1593;
Best Local Similarity 57.4%; Pred.No.17e-41;
Matches 410; Conservative 0; Mismatches 292; Indels 12; Gaps 3;

QY 784 ACTTCACATACGAGAGCTAGAGCCAAATGTTCTCCGAGCGAATTGTTA 843
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DB 226 AATTCACTTCCTCGGAGCTTCAGCTGCACAAACAAATTAGCCCTATTGTTGCTA 285

QY 844 GGACAAAGCGGCTTGCTTACGTGCAAAAGGTGTTGCTT---AGTGGAAAGACT 900
   |||||
DB 286 GGAGAAAGGCGGCTTGCTTACGTGCAAAAGGTGTTGCTT---AGTGGAAAGACT 900

QY 901 GGTGGAAGCAATGTAAGTTGGAGTGTGAGGAGAGAGAGTTTCAGAGAGAGTT 960
   |||||
DB 346 GCTGTCAACCAATTGATGATGGAACGCGGCTGCAGGAGTACCGTGATTTCTGTAAGATT 405

QY 961 GAGATCATCGAGAGATTCACCAAGGCAATGCTGTGCTCTTGTGGTATTGATCGCC 1020
   |||||
DB 406 CTTATGCTCAGCTTTTACATCATCCCAATTGGTGAATTTAATGGATTAAGTGTGAT 465

QY 1021 GGTGCAAAAGATTGCTTCTATGATGTTGTTCTTAACAACATTCGAGCTTACCTC 1080
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DB 466 GGTGCAAAAGCTTCTGTTTATGATTCATGATCCCATTTGGGATTCGTAAGAATCATCTT 525

QY 1081 CATGGAGAGGAGCGGCTTA-----CAATGATGAGAGACAGAGATTGAAGTGTCTCT 1134
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DB 526 CATGATCTCCCAACGAAAGAAAGAGCGCTTAAGTTGGAACAAAGATTAAGTATAGCGCT 585

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QY 1135 GGATCTGCTAAAGACTTTCTTATCTTCATGAGATTGCANCTTAAATCATTCACCGT 1194  
DB 586 GGTGACAGTCAGAGTTTGGATTTCTTACGATAGAGTAATCTCCCTGTTATTTACAG 645  
QY 1195 GATATCAAGGCTTCAACATATATGATGATTTCAGATTGAGAGTTGCTGATTTT 1254  
DB 646 GATTTCATATATCAACATTTTGTCTCGTAGGGATTTCAACCAACCTTTTCATTTTC 705  
QY 1255 GGTCTGTGTAGATG---CTTCTGATACAAACCGCATATATCAACGCTGATGGGA 1311  
DB 706 GGGCTAGGAGATTGGCCCGCAGAGATAGTTTCAATGATCCACGCGTCAATGGGA 765  
QY 1312 ACCTTTGGGTAAGTCTGCTCCGGAATACGCTGCAAGCGGAAGCTCAACGAGATGAC 1371  
DB 766 ACGATAGTACTGCTGCTCGAGATAGCATGACCGGTCACACTACGTTAAGTCAT 825  
QY 1372 GTTTTCTATTTGGGCTGTGCTTTGAGACTCATTTACGACGTCGACCGCTGATGCC 1431  
DB 826 GTGATAGCTTTGGGCTGTGCTTTCTTACGCTTATACAGCGCGAAGGCAATTCACAGC 885  
QY 1432 AACATGCTATGATGATGACAGCTTATGACTGCGGACGACCATTCCTTAAC 1485  
DB 886 AGTGACCGCAGAGACAGACATCTGCTCACTTGGGACACACCTTATTCAAC 939

## RESULT 2

US-10-101-464A-886  
; Sequence 886, Application US/10101464A  
; Patent No. 6768041  
; GENERAL INFORMATION:  
; APPLICANT: Strabala, Timothy  
; APPLICANT: Nieuwenhuizen, Nicolaas  
; APPLICANT: Higgins, Colleen M.  
; TITLE OF INVENTION: Compositions Isolated from Plant Cells  
; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling  
; FILE REFERENCE: 11000.1020C2  
; CURRENT APPLICATION NUMBER: US/10/101,464A  
; PRIOR FILING DATE: 2002-03-18  
; PRIOR APPLICATION NUMBER: 09/704,302  
; PRIOR FILING DATE: 2000-11-01  
; PRIOR APPLICATION NUMBER: 09/228,986  
; PRIOR FILING DATE: 1999-01-12  
; PRIOR APPLICATION NUMBER: 60/162,866  
; PRIOR FILING DATE: 1999-11-01  
; PRIOR APPLICATION NUMBER: PCT/US00/00724  
; PRIOR FILING DATE: 2000-01-11  
; NUMBER OF SEQ ID NOS: 989  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 886  
; LENGTH: 3108  
; TYPE: DNA  
; ORGANISM: Eucalyptus grandis  
US-10-101-464A-886

Query Match 9.9%; Score 192.4; DB 4; Length 3108;  
Best Local Similarity 53.9%; Pred. No. 3.2e-41;  
Matches 419; Conservative 0; Mismatches 356; Indels 3; Gaps 1;

QY 787 TTCACATCGAGAGCTAGTAGAGCCACCAATGTTTCTCCGAGGCAACTGTTAGGA 846  
DB 1881 TACCATTACGGCGCATTTGAAGAGCTACGAATATTTTAAAGGAAGATTGATTAATAGG 1940  
QY 847 CAAGCGGGGTTTGGTTACGTGCACAAAGTGTTGCTTACGAGGAAGAAGTTGCTGTG 906  
DB 1941 ACGGAGGTTTGGGAAAGTCTACAAAGGAATTTTCAAGATGGGACCTAAGGTGCAAGTG 2000  
QY 907 AAGCATTTGAAGTTGGAGTGTCAGAGGAGAGAGAGGAGTTTCAGGACAGGTTGATC 966  
DB 2001 AAGAGGGGCAATCCAAAGTCCCAACAGGGGCTGACGGAGTTCCGTAACGAATCGAGATG 2060  
QY 967 ATCAGCAGAGTTTACCAAGGATCTGTTGCTCTTGTGTTATGATGCGCGGTGCC 1026

DB 2061 TTGCTCAGATTTCGACCGCCATCTGATGCTGATTCGGGTATATTCGACGAACGAAT 2120  
QY 1027 AAAAGATTGCTGTGCTATGAGTTTGTCTTACAAACAATCTCGAGCTTCACTCCATGAGC 1086  
DB 2121 GAGATGATCATCATCTATGAATTCATGAAACCGGACCTTTAAGATCATCTGATCTGT 2180  
QY 1087 GAGGAGCGGCTTACATGAAATGAGAGCAACGATTTGAAGATTTGCTGTTGATCTGATAA 1146  
DB 2181 TCGGATGCTCCGTCGTGATGAGTTGAGAGCAAGGCTGAGATTTGATGAGGTGAGCTAA 2240  
QY 1147 GGACTTTCTTATCTTTCATGAAAGATTGCAATCTTAAATCATTCACCGGATATCAAGCT 1206  
DB 2241 GGGCTTCACTACCTTTCACACCGGCTCCACAAAGGCAATCATCTCGGAGTCAAGTCG 2300  
QY 1207 TCAACATATGATGATGATTTCAAGTTGAAGCTGATGCTGATTTGTCTGCTGAAG 1266  
DB 2301 GCAATATCTCTTTGATGAGAAATTTGATGSCCAAGTTGCCGATTTGGGCTGCAAG 2360  
QY 1267 ATTGCTTCTGATACAAAC--ACGCAATGATCAACAGCTGTGATGGAACTTTGGGTAC 1323  
DB 2361 ACCGCTCTGAGATGACACGACGACGACGACGACGACGACGACGACGACGACGACGAT 2420  
QY 1324 TTGGCTCCGGAATACGCTGCAAGGGAAGTCAACGAGAGTCTGACGTTTCTCATTT 1383  
DB 2421 CTGATCTGATACCTGACGAGGCAACGCTCAAGGAAATATCATGATCTACTCATTC 2480  
QY 1384 GCGCTGTGCTTTTGAAGCTTACTGACGCTGACCGCTGTGATGCCAAGATCTAT 1443  
DB 2481 GGGGTCTGATGCTTGAATCTCTTGTGTAGACGGTATTCGATCCGCTGCCAGGA 2540  
QY 1444 GTAGATGACAGCTTAGTTGACTGGGACGACCATTTCTTAAACGAGATCTGAGCAAGA 1503  
DB 2541 GAAAGGGAATTTAGTTGATGAGTGCGCAATGAAATGCGCAGAAAGAGGCGAATCCAA 2600  
QY 1504 GACTTGAAGGTTTATGCTGATGCAAGATGATATGCTATGACAGAGAGAGATG 1561  
DB 2601 ACCATTAACCTCATCTTGTGCTCAAGCAATGAAGATCCCTCTGGAAGTTGCTGG 2658

## RESULT 3

US-09-228-986-4  
; Sequence 4, Application US/09228986  
; Patent No. 6359198  
; GENERAL INFORMATION:  
; APPLICANT: Strabala, Timothy  
; APPLICANT: Nieuwenhuizen, Niels  
; TITLE OF INVENTION: Compositions Isolated from Plant Cells  
; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling  
; FILE REFERENCE: 11000/1020  
; CURRENT APPLICATION NUMBER: US/09/228,986  
; PRIOR FILING DATE: 1999-01-12  
; NUMBER OF SEQ ID NOS: 130  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 4  
; LENGTH: 2868  
; TYPE: DNA  
; ORGANISM: Pinus radiata  
US-09-228-986-4

Query Match 9.4%; Score 182; DB 3; Length 2868;  
Best Local Similarity 52.9%; Pred. No. 1.9e-38;  
Matches 467; Conservative 0; Mismatches 400; Indels 15; Gaps 3;

QY 787 TTCACATCGAGAGCTAGTAGAGCCACCAATGTTTCTCCGAGGCAACTGTTAGGA 846  
DB 1116 TTTCATTAACGGGAATTAAGAGTTGCAATGATGTTTAAAGATTAAGAAATCTTGTGC 1175  
QY 847 CAAGCGGGGTTTGGTTACGTGCACAAAGTGTGTTGCTTAAGTGGAAAGAAAGTTGCTGTG 906  
DB 1176 AAGAGTGTGTTTGGAAAGGTATACAAAGGGGCTTGCAGATGTTCTTGTGTGCTGTGA 1235  
QY 907 AAGCATTTGAAGTTGGAGTGTCAG--GGAAGAGAGGATTTCAAGCAGAGTTGAG 963

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Db      1236 AAACGCTGGAAGAAAGACGTAACCGGGTGGAGAGTTGCAAGTTTCAACAGAAATGGAG 1295
Qy      964 ATCATCAGCAGAGTTTACCAACAGAGCATGTGATGCTCTTTGTTGTTATTTGATCGCCGGT 1023
Db      1286 ATGATTAAGCATGAGCATATAGAAACCTCTTCCAGTACAGGATTTCTGATGACACC 1355
Qy      1024 GCCAAAGATTGCTTCTATGAGTTTGTCTTAAACAATCTCGAGCTTCACCTGCAT 1083
Db      1356 ACTGAACCGCTGCTGTTATATCCATACATGCGCATGAGAGTTGCTTCAATGCTTACGA 1415
Qy      1084 GCGGAGGAGC-----GGCTTAACATGATGAGACCAACAATTGAAGATTGCTTGGGA 1137
Db      1416 GAGAGGACCAAAATGACCCACCTTAATGAGCCAACTCGACAGGATGATGGAT 1475
Qy      1138 TCTGCTAAAGACATTCTTATCTTCATGATGATGATGATGATGATGATGATGATGATGAT 1197
Db      1476 TCTGCAAGAGGCTCTCTCTACTGATGATGATGATGATGATGATGATGATGATGATGAT 1535
Qy      1198 ATCAAGGCTTCAACATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1257
Db      1536 GTCAAGGCTGCTAAATCTTACTGATGATGATGATGATGATGATGATGATGATGATGAT 1595
Qy      1258 CTGCTAAGATTGCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1317
Db      1596 TTGGCAAACTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1655
Qy      1318 GGGTACTTGCTCCGGAATACGCTGCAAGCGGAAGCTCAAGAGATGCTGACCTTTTC 1377
Db      1656 GCGCAATAGACCTGAGTACCTTTCTATGATGATGATGATGATGATGATGATGATGAT 1715
Qy      1378 TCATTTGCGGTTGCTTTTGGAGCTTACTTATGATGATGATGATGATGATGATGATGAT 1437
Db      1716 GGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1769
Qy      1438 GTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1497
Db      1770 GCACGTTTGAACAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1829
Qy      1498 CAAGAGACCTTTGAGGTTTATGCTGATGATGATGATGATGATGATGATGATGATGAT 1557
Db      1830 GAGAAAGGCTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1889
Qy      1558 ATGCTCGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1617
Db      1890 GTGGAACAACCTTATCAAGTGTACTTATGATGATGATGATGATGATGATGATGAT 1949
Qy      1618 CGCATGAGCAGATTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1659
Db      1950 AAGATGCTGAAGTGTGAAGATGTTGGAAGGGATGGCTTA 1991

RESULT 4
US-10-101-464A-4
; Sequence 4, Application US/10101464A
; Patent No. 678041
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Nicolaas
; APPLICANT: Higgins, Colleen M.
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; TITLE OF INVENTION: and their Use in the Modification of Plant Cell Signaling
; FILE REFERENCE: 11000.1020C2
; CURRENT APPLICATION NUMBER: US/10/101,464A
; PRIOR FILING DATE: 2002-03-18
; PRIOR APPLICATION NUMBER: 09/704,302
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 09/228,986
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/162,866
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: PCT/US00/00724
; PRIOR FILING DATE: 2000-01-11
; NUMBER OF SEQ ID NOS: 989

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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 2868
; TYPE: DNA
; ORGANISM: Pinus radiata
US-10-101-464A-4

Query Match      9.4%; Score 182; DB 4; Length 2868;
Best Local Similarity 52.9%; Pred.No. 1.9e-38;
Matches 467; Conservative 0; Mismatches 400; Indels 15; Gaps 3;

Qy      787 TTGACATPACAGAGAGCTAGTACAGCCCAATGTTTCTCGAGGCGCACTTTGATGA 846
Db      1116 TTCTCATTAACGGGAATTAACAGTTTCACTGATGATGATGATGATGATGATGATGAT 1175
Qy      847 CAAGCGGCTTCCGTTACGTCACAAAGGTTGTTGCTAGTGGGAAAGATTGCTGTG 906
Db      1176 AGAGTGGTTTGGAAAGGTGTACAAAGGGCGCTTGAGATGATGATGATGATGATGATGAT 1235
Qy      907 AAGCATGAAAGTTGGAGTGTGAG---GAGAGAGGAGTTTCAAGGCAAGGTTGAG 963
Db      1236 AAACGCTGGAAGAAAGACGTAACCGGGTGGAGAGTTGCAAGTTTCAACAGAAATGGAG 1295
Qy      964 ATCATCAGCAGAGTTTACCAACAGAGCATGTGATGCTCTTTGTTGTTATTTGATCGCCGGT 1023
Db      1296 ATGATTAAGCATGAGCATATAGAAACCTCTTCACTACATGATGATGATGATGATGAT 1355
Qy      1024 GCCAAAGATTGCTTCTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1083
Db      1356 ACTGAACGCTGCTGTTGTTATCTTACATGAGCCAAATGGAAGTGTGCTTCAAGCTTACGA 1415
Qy      1084 GCGGAGGAGC-----GGCTTAACATGATGAGACCAACAATTGAAGATTGCTTGGGA 1137
Db      1416 GAGAGGACCAAAATGACCCACCTTAATGAGCCAACTCGACAGGATGATGGAT 1475
Qy      1138 TCTGCTAAAGACATTCTTATCTTCATGATGATGATGATGATGATGATGATGATGATGAT 1197
Db      1476 TCTGCAAGAGGCTCTCTCTACTGATGATGATGATGATGATGATGATGATGATGATGAT 1535
Qy      1198 ATCAAGGCTTCAACATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1257
Db      1536 GTCAAGGCTGCTAAATCTTACTGATGATGATGATGATGATGATGATGATGATGATGAT 1595
Qy      1258 CTGCTAAGATTGCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1317
Db      1596 TTGGCAAACTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1655
Qy      1318 GGGTACTTGCTCCGGAATACGCTGCAAGCGGAAGCTCAAGAGATGCTGACCTTTTC 1377
Db      1656 GCGCAATAGACCTGAGTACCTTTCTATGATGATGATGATGATGATGATGATGATGAT 1715
Qy      1378 TCATTTGCGGTTGCTTTTGGAGCTTACTTATGATGATGATGATGATGATGATGATGAT 1437
Db      1716 GGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1769
Qy      1438 GTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1497
Db      1770 GCACGTTTGAACAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1829
Qy      1498 CAAGAGACCTTTGAGGTTTATGCTGATGATGATGATGATGATGATGATGATGATGAT 1557
Db      1830 GAGAAAGGCTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1889
Qy      1558 ATGCTCGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1617
Db      1890 GTGGAACAACCTTATCAAGTGTACTTATGATGATGATGATGATGATGATGATGAT 1949
Qy      1618 CGCATGAGCAGATTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1659
Db      1950 AAGATGCTGAAGTGTGAAGATGTTGGAAGGGATGGCTTA 1991

RESULT 5

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US-09-579-182-4
; Sequence 4, Application US/09579182
; Patent No. 650628
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN KINASE AND
; FILE REFERENCE: NMI-161
; CURRENT APPLICATION NUMBER: US/09/579,182
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 1488
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-579-182-4

Query Match          9.2%; Score 179.8; DB 4; Length 1488;
Best Local Similarity 53.8%; Pred. No. 4.9e-38;
Matches 470; Conservative 0; Mismatches 382; Indels 21; Gaps 4;

QY 784 ACTTTCATACGAGCGAGTGTAGAGCCACCAATGGTTTCTCCGAGCGAAGTTGTA 843
DB 154 ACCTTTACTTCCGAGAGTTAGCTGCCGCACTAAAACTTTCGACCGGAATGTTCTT 213
QY 844 GAGACAGGCGGTTCCGTTACGTGCACAAAG--GTGTGTCTCTAGTGGGAAAGATT 900
DB 214 GGAAGAGAGGTTTCGACGCTTTACAAAGTGTCTAGAGACACACAGCAATAGTA 273
QY 901 GCTGTGAAGAGTTGAAAGTTGGAGTGTGAGGAGAGAGAGAGTTTACGACAGAGTT 960
DB 274 GCTGTGAAGAGTTGAAAGTTGGAGTGTGAGGAGAGAGAGAGTTTACGACAGAGTT 333
QY 961 GAGATCATACGAGAGTTTACCAAGAGATGATGATGATGATGATGATGATGATGATG 1020
DB 334 CTATGCTGAGCCTTCTGACATCAATCTTGTGAATTTGATTTGATTTGCTGAT 393
QY 1021 GGTGCAAAAGATTTGCTGATGATGATGATGATGATGATGATGATGATGATGATG 1080
DB 394 GGGAGCAGAGGCTTCTGTTGATGATGATGATGATGATGATGATGATGATGATGATG 453
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DB 634 GGGTTACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 693
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DB 867 --AGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 924

US-09-228-986-9
; Sequence 9, Application US/09228986
; Patent No. 6359198
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; FILE REFERENCE: 11000/11020
; CURRENT APPLICATION NUMBER: US/09/228,986
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 3239
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-09-228-986-9

Query Match          9.2%; Score 178.4; DB 3; Length 3239;
Best Local Similarity 55.9%; Pred. No. 1.8e-37;
Matches 360; Conservative 0; Mismatches 281; Indels 3; Gaps 1;

QY 787 TTCATATACGAGAGCTAGCTAGAGCCACCAATGGTTTCTCCGAGCGCAATTTGTAGA 846
DB 2026 TTCTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2085
QY 847 CAAGCGCGGTTTCGTTACGTGCACAAAGTGTGTGCTAGTGGGAAAGAGTTGCTGTG 906
DB 2086 TTCCGAGAGATACGAAAGGTGTACAGGAGGATTTCTCTGATGATGATGATGATG 2145
QY 907 AAGCATTTGAAAGTTGGAGTGTGTCAGGAGAGAGGAGTTTACGAGCAGAGTTGATGC 966
DB 2146 AAAAGACTGACAGAGGAGTGCATGACAGGATGCAACGAGTTCAAGACAGAAATGAG 2205
QY 967 ATGACGAGATTCACCAACAGCATGTGTCTTCTTGTGTTATGTCATGCGCGGTGCC 1026
DB 2206 CTTTCGGGGTTTCAATCAAGAAATCTTGTGGCTCATAGATTTCTGTTTCAGACAA 2265
QY 1027 AAAAGATTTGCTGCTATGATGATGATGATGATGATGATGATGATGATGATGATG 1086
DB 2266 GAGAGATTTGCTGCTATGATGATGATGATGATGATGATGATGATGATGATGATG 2325
QY 1087 GAGGAGCGGCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATG 1146
DB 2326 AAATCAGGATTTATCTTGAATGGAAGAGAGGCTTGATGATGATGATGATGATG 2385
QY 1147 GGAATTTCTTATCTTCAATGATGATGATGATGATGATGATGATGATGATGATG 1206
DB 2386 GGAATCTTATCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATG 2445
QY 1207 TCAAAATATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1266
DB 2446 ACCAATATCTTGTGAGAGCAATCTGACGCGCAAAATGCGGATTTCCGATTTCCAAA 2505
QY 1267 ATTGCTTCTGATA--CAAAACGATGATGATGATGATGATGATGATGATGATGATG 1323
DB 2506 CTGCTATCGACAGCGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2565
QY 1324 TTGCTGCGGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1383
DB 2566 TTGATCCGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2625
```





Db 760 CCGACTTCGGGCTCGCGAAACTGGAGCCCACTGGAGACAACTGATGTTCCACAGCGG 819  
QY 1304 TGAAGGGAACCTTTGGGACTTGGCTCCGGATACGCTGCAGAGGGAAGCTCAGAGA 1363  
Db 820 TGAAGGGGACATGAGCTTACGCTCTCTGAGTAGCCATGACGTCAGTTAAAGCGCA 879  
QY 1364 AGCTGACGTTTCTCATTTTGGCGCTTGTGCTTTTGAAGCTCATTAAGTGAAGTGCACCG 1423  
Db 880 AATCGATGTGTACAGCTTGTGTGTGTCTTTTGAAGCTTATTAAGCGTGAAGAAAGCA 939  
QY 1424 TTGATGCCAACAATGTCTATGTATGATGACAGCTTAGTTGACCTGGCAGCAAGCAATGCTTA 1483  
Db 940 TAGATAGACTCAACACATGAGAGAGAACTGTGTACATGGGACAGACTTGTGTTCA 999  
QY 1484 AC 1485  
Db 1000 AC 1001

RESULT 9  
US-09-228-986-7  
; Sequence 7, Application US/09228986  
; Patent No. 6359198  
; GENERAL INFORMATION:  
; APPLICANT: Strabala, Timothy  
; APPLICANT: Nieuwenhuizen, Niels  
; TITLE OF INVENTION: Compositions Isolated from Plant Cells  
; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling  
; FILE REFERENCE: 11000/1020  
; CURRENT APPLICATION NUMBER: US/09/228,986  
; CURRENT FILING DATE: 1999-01-12  
; NUMBER OF SEQ ID NOS: 130  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 7  
; LENGTH: 2432  
; TYPE: DNA  
; ORGANISM: Pinus radiata  
US-09-228-986-7

Query Match 9.0%; Score 174.6; DB 3; Length 2432;  
Best Local Similarity 56.5%; Pred. No. 1.6e-36;  
Matches 368; Conservative 0; Mismatches 274; Indels 9; Gaps 2;  
QY 787 TTCACATACGAGAGCTAGTAGAGCCACCAATGGTTCTCCGAGCGAAGCTGTAGGA 846  
Db 1070 TTCTCATTAAGAGGTTACGTTTCCACTATATTTTACTAGCAGAAATATTTAGGA 1129  
QY 847 CAAGCGCGGTTGCTTACGTGACCAAAAGTGTGCTTACGAGGAAAGAGTTGCTGTG 906  
Db 1130 GTAGAGAGATATGATGTCTATTAAGGATTCTTCAAGATGGCACTATATGACATA 1189  
QY 907 AAGAGTTGAAGTTGGAGT--GTCAGGAGAGAGAGGAGTTTCAGGAGAGTTGAG 963  
Db 1190 AAAAGTTGAAGATGTAATGTGTGAGAGAGAGAAATTCATTTCAACAGAGGTGAA 1249  
QY 964 ATCATACGAGAGTTCAACACAGGCAATCTGTGTCTCTTGTGTTATGATGCGCGT 1023  
Db 1250 ATGATACGCTTGGCTGTCATAGGAACCTATTAAGATGTATGATTTTGAACAACCTCC 1309  
QY 1024 GCCAAAAGATTGCTTGTCTATAGAGTTGTTCTTAACAACAATCTCG-----AGCTTAC 1077  
Db 1310 AGAGAGAGGCTTCTGTCTATCCCTACATGCAATGGAATGTGTGCTTGTGTTAGA 1369  
QY 1078 CTCATGCGGAGGAGCGGCTTACATGGAATGAGACACAGATTGAAGATTGCTTTGGA 1137  
Db 1370 GATCATATTAATGAAAAGCTTCCCTGAGCTTGGCTTACGCAAGCGTATAGCCTTTGGA 1429  
QY 1138 TCTGCTAAAGAGCTTTTATCTTATCTTCAAGAGATTGCAATCTTAATCAATCAACGCTGAT 1197  
Db 1430 GCACTAGGAGGAGCTGTATATTTTGCATGACAGCAATGTATCCCAAGATTATTCACCGGAT 1489  
QY 1198 ATCAAGGCTTCAACATATTAATGATTAATTTCAAGTTGAAGCTAAAGTTGCTGATTTGGT 1257

Db 1490 GTGAAGCAGAAATATATTAATCTAGTGAATATTTGAAGCTGTGTGAGATTTGGG 1549  
QY 1258 CTCTCTAGATGTCTTGTGATCAAAACGCAATGATATCAACAGTGTGATGGAACTTT 1317  
Db 1550 TTACAAAGCTCTTGATTCACAGGAGATTCATGTGACTACTGTCTTCAGGAGCGGTA 1609  
QY 1318 GGGTACTTGGCTCCGGAATACGCTGCAAGCGGAAAGCTCAAGGAAAGTCTGACGTTTC 1377  
Db 1610 GGTACATTTGCCCAATATCTTTCAACGAGGACAAATCTTCAAGAAATGATGATTT 1669  
QY 1378 TCATTTGCGCTTGTGCTTTTGGAGCTCATTACTGACGTCGACCGCTGAT 1428  
Db 1670 GCGTTGGATATTAATGATTTGGAATCTATTAACAGACAAAGGCTTTAGAT 1720

RESULT 10  
US-10-101-464A-7  
; Sequence 7, Application US/10101464A  
; Patent No. 6768041  
; GENERAL INFORMATION:  
; APPLICANT: Strabala, Timothy  
; APPLICANT: Nieuwenhuizen, Nicolaas  
; APPLICANT: Higgins, Colleen M.  
; TITLE OF INVENTION: Compositions Isolated from Plant Cells  
; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling  
; FILE REFERENCE: 11000.1020c2  
; CURRENT APPLICATION NUMBER: US/10/101,464A  
; PRIOR APPLICATION NUMBER: 09/704,302  
; PRIOR FILING DATE: 2000-11-01  
; PRIOR APPLICATION NUMBER: 09/228,986  
; PRIOR FILING DATE: 1999-01-12  
; PRIOR APPLICATION NUMBER: 60/162,866  
; PRIOR FILING DATE: 1999-11-01  
; PRIOR APPLICATION NUMBER: PCT/US00/00724  
; PRIOR FILING DATE: 2000-01-11  
; NUMBER OF SEQ ID NOS: 989  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7  
; LENGTH: 2432  
; TYPE: DNA  
; ORGANISM: Pinus radiata  
US-10-101-464A-7

Query Match 9.0%; Score 174.6; DB 4; Length 2432;  
Best Local Similarity 56.5%; Pred. No. 1.6e-36;  
Matches 368; Conservative 0; Mismatches 274; Indels 9; Gaps 2;  
QY 787 TTCACATACGAGAGCTAGTAGAGCCACCAATGGTTCTCCGAGCGAAGCTGTAGGA 846  
Db 1070 TTCTCATTAAGAGGTTACGTTTCCACTATATTTTACTAGCAGAAATATTTAGGA 1129  
QY 847 CAAGCGCGGTTGCTTACGTGACCAAAAGTGTGCTTACGAGGAAAGAGTTGCTGTG 906  
Db 1130 GTAGAGAGATATGATGTCTATTAAGGATTCTTCAAGATGGCACTATATGACATA 1189  
QY 907 AAGAGTTGAAGTTGGAGT--GTCAGGAGAGAGGAGTTTCAGGAGAGTTGAG 963  
Db 1190 AAAAGTTGAAGATGTAATGTGTGAGAGAGAGAAATTCATTTCAACAGAGGTGAA 1249  
QY 964 ATCATACGAGAGTTCAACACAGGCAATCTGTGTCTCTTGTGTTATGATGCGCGT 1023  
Db 1250 ATGATACGCTTGGCTGTCATAGGAACCTATTAAGATGTATGATTTTGAACAACCTCC 1309  
QY 1024 GCCAAAAGATTGCTTGTCTATAGAGTTGTTCTTAACAACAATCTCG-----AGCTTAC 1077  
Db 1310 AGAGAGAGGCTTCTGTCTATCCCTACATGCAATGGAATGTGTGCTTGTGTTAGA 1369  
QY 1078 CTCATGCGGAGGAGCGGCTTACATGGAATGAGACACAGATTGAAGATTGCTTTGGA 1137  
Db 1370 GATCATATTAATGAAAAGCTTCCCTGAGCTTGGCTTACGCAAGCGTATAGCCTTTGGA 1429

QY 1138 TCTGCTAAGAGACTTCTTATCTTCATGAGAGATGCAATCCTAATAATCATACCGGTAT 1197  
 DB 1430 GCAGCTAGGGAGCTGTATATTTGATGATGAGCAATGTGATCCCAAGATTAATTCACCGGAT 1489  
 QY 1138 ATCAAGGCTCAACATATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1257  
 DB 1490 GTGAAGAGAGCAAAATATATTTACTGATGATGATGATGATGATGATGATGATGATGATGAT 1549  
 QY 1258 CTGCTAGATGCTCTTCTGATACAAACAGCATGTATCAACAGCTGATGATGATGATGATGAT 1317  
 DB 1550 TTAGCAAGAGCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1609  
 QY 1318 GGGTACTGCTCCGGAATACGCTGCAAGCGGAAGCTCAGGAGAAAGTCTGATGATGATGATGAT 1377  
 DB 1610 GGTGACATTTGCCCGGAAATACCTTTCAAGGAGCAATCTTCAAGAGAAAGATGATGATGAT 1669  
 QY 1378 TCAATTTGGCGTTGCTTGTGCTTTGAGAGCTCATTTACTGAGCTGACCGGTGAT 1428  
 DB 1670 GGCTTTGGGATATTTACTGTTGGAATCATTTACAGAGCAAGGGCTTTGAT 1720

## RESULT 11

US-10-101-464A-159  
 ; Sequence 159, Application US/10101464A  
 ; Patent No. 6768041  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Strabala, Timothy  
 ; APPLICANT: Nieuwenhuizen, Nicolaas  
 ; APPLICANT: Higgins, Colleen M.  
 ; TITLE OF INVENTION: Compositions Isolated from Plant Cells  
 ; FILE REFERENCE: 11000.1020c2  
 ; CURRENT APPLICATION NUMBER: US/10/101,464A  
 ; PRIOR FILING DATE: 2002-03-18  
 ; PRIOR APPLICATION NUMBER: 09/704,302  
 ; PRIOR FILING DATE: 2000-11-01  
 ; PRIOR APPLICATION NUMBER: 09/228,986  
 ; PRIOR FILING DATE: 1999-01-12  
 ; PRIOR APPLICATION NUMBER: 60/162,866  
 ; PRIOR FILING DATE: 1999-11-01  
 ; PRIOR APPLICATION NUMBER: PCT/US00/00724  
 ; PRIOR FILING DATE: 2000-01-11  
 ; NUMBER OF SEQ ID NOS: 989  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 159  
 ; LENGTH: 1457  
 ; TYPE: DNA  
 ; ORGANISM: Eucalyptus grandis  
 US-10-101-464A-159

Query Match 8.9%; Score 173; DB 4; Length 1457;  
 Best Local Similarity 55.6%; Pred. No. 3.2e-36;  
 Matches 354; Conservative 0; Mismatches 280; Indels 3; Gaps 1;

QY 784 ACTTTCACATACAGAGAGTAGTACAGAGCAAGTCTTCTCCAGGCGAATCTGTTA 843  
 DB 70 AATTTCAGACTCTCTACCTTTGAGAGGCCAGGATCTTTTACAGCGCAATTAAGCTC 129  
 QY 844 GGAAGAGCGGCTTGGTTACGTCACAAAGGTGTGTTGCTTGAAGGAAAGATTGCT 903  
 DB 130 GGCAGAGTGGATTTGGCACTGTCTATTAAGGAGTTCTTCTGATGAGAGGAGATGCT 189  
 QY 904 GTGAAGACAGTGAAGAGTGGAGTGTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 963  
 DB 190 GTTAAAGAGCTCTTCTTCAACATTAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 249  
 QY 964 ATCATCAGAGAGATTCACAG 1023  
 DB 250 ATTAATAGAGAGTGTGAG 309  
 QY 1024 GCCAAAGATGCTTGTCTATGAGATTGTCTTACAGAGAGATCTGAGCTTAC--CTC 1080  
 DB 310 CCGAAGAGCTTCTTGTCTATGAGTTCTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 369

QY 1081 CATGGCGAGGAGCGGCTTCAATGAGATGAGAGACACAGATTTGAGATGCTCTGGAGTCT 1140  
 DB 370 GATGCAACCAAG 429  
 QY 1141 GCTAAAGAGCTTCTTATCTTCAATGAGATGAGATGAGATGAGATGAGATGAGATGAGAT 1200  
 DB 420 GCAGAGGTTGGATATCTTCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 489  
 QY 1201 AAGGCTCAACATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1260  
 DB 490 AAGGAGATATATCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 549  
 QY 1261 GCTAAGATGCTTCTGATACAAACAGCATGATACACAGCTGATGATGATGATGATGATGAT 1320  
 DB 550 GCCAGATTTCTCCAG 609  
 QY 1321 TACTTGGCTCCGGAATACGCTGCAAGCGGAAGCTCAGGAGAGAGAGAGAGAGAGAGAGAG 1380  
 DB 610 TATATGCTCCAGAGATCCTAGCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 669  
 QY 1381 TTGGCGTGTGCTTTTGGAGCTCATTTACTGAGAGCTC 1417  
 DB 670 TATGATGCTCTTCTGAG 706

## RESULT 12

US-10-101-464A-461  
 ; Sequence 461, Application US/10101464A  
 ; Patent No. 6768041  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Strabala, Timothy  
 ; APPLICANT: Nieuwenhuizen, Nicolaas  
 ; APPLICANT: Higgins, Colleen M.  
 ; TITLE OF INVENTION: Compositions Isolated from Plant Cells  
 ; FILE REFERENCE: 11000.1020c2  
 ; CURRENT APPLICATION NUMBER: US/10/101,464A  
 ; PRIOR FILING DATE: 2002-03-18  
 ; PRIOR APPLICATION NUMBER: 09/704,302  
 ; PRIOR FILING DATE: 2000-11-01  
 ; PRIOR APPLICATION NUMBER: 09/228,986  
 ; PRIOR FILING DATE: 1999-01-12  
 ; PRIOR APPLICATION NUMBER: 60/162,866  
 ; PRIOR FILING DATE: 1999-11-01  
 ; PRIOR APPLICATION NUMBER: PCT/US00/00724  
 ; PRIOR FILING DATE: 2000-01-11  
 ; NUMBER OF SEQ ID NOS: 989  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 461  
 ; LENGTH: 2175  
 ; TYPE: DNA  
 ; ORGANISM: Eucalyptus grandis  
 US-10-101-464A-461

Query Match 8.7%; Score 168.2; DB 4; Length 2175;  
 Best Local Similarity 55.9%; Pred. No. 7.8e-35;  
 Matches 364; Conservative 0; Mismatches 278; Indels 9; Gaps 2;

QY 780 AACCTTTCACTACAGAGAGTACAGAGCAATGATTTCTCGAGGCGAATCTT 839  
 DB 968 AAGAGAGTTCACCTTCAAGGAACTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1027  
 QY 840 GTTAAAG 899  
 DB 1028 GATGAG 1087  
 QY 900 TGCTGTGAAG 956  
 DB 1088 TGGAGATCAAG 1147  
 QY 957 GGTGAGATCATCAG 1016

Db 1148 ACTGAGATGATGACCTAGGGGTGACCGCAACCTTCTGGCTCTATGATTTGTAT 1207  
Qy 1017 GCCCGGTGCAAAAGATTGCTTGTCTATGAGTTTGTCTTACCAACATCTGACCTTCA 1076  
Db 1208 GACCCAAACGGAGAGCTTCTGTATACCCCTACATGTCACACGCGAGTGGCACTCG 1267  
Qy 1077 CCTCATGCGGAGGAGCGGCTTACATGAGATGAGACACCAATGAGATTGCTCTTGG 1136  
Db 1268 TCTCAGAGCCAA-----ACCAACCTTGGAGTGGAGCAACAGAAAAGATTGCTTGG 1321  
Qy 1137 ATCTGCTAAGAGACTTCTTATCTTCATGAGATTGCAATCTTAAATCATTCACCGTCA 1196  
Db 1322 GCGAGCAAGGAGCTTGTATCTGACGACAGCAATGTGACCCCAATATATCATAGGCA 1381  
Qy 1197 TATCAAGCTTCAACATATGATATGATTTCAAGTTGAAGTGAAGTTGCTGATTTGG 1256  
Db 1382 TGTTAAGGGGAGGAGACATATGCTTACACGACTACGGAAGCTGTGTGGAGACTTGG 1441  
Qy 1257 TCTGTGTAAGATTGCTTGTATCAAAACGACATGTATCAACAGCTGTATGAGGAACTT 1316  
Db 1442 ATTGCAAGCTTGTGATCATGAGGAATCCACGTGACCAACCGCGTGAAGGCGACAGC 1501  
Qy 1317 TGGTACTTGGCTCCGAAATAGCTGCAAGCGGAAAGCTTACGAGAGAGTCTGACCTTT 1376  
Db 1502 AGGGGACATTTGCTCCAGAGTACTTAAAGCGGAGCTCTCTGAGAAAAACGATGTTTT 1561  
Qy 1377 CTGATTTGGCGTGTGCTTTTGGAGTCAATTAAGTCTGACGCGACCGGTTGA 1427  
Db 1562 TGGGTTTGAATCTTCTGCTGCACTGATTAAGTCTGAGAGCTCTTGA 1612

RESULT 13  
US-08-265-628-1  
Sequence 1, Application US/08265628  
Patent No. 5821094  
GENERAL INFORMATION:  
APPLICANT: Roche/Stein, Steven J.  
TITLE OF INVENTION: S-LOCUS RECEPTOR KINASE GENE IN A  
TITLE OF INVENTION: SELF-INCOMPATIBLE BRASSICA NAPUS LINE  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
STREET: 500 W. Madison St. Suite 3400  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60661  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/265,628  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/959,945  
FILING DATE:  
APPLICATION NUMBER: US 07/847,564  
FILING DATE: 03-MAR-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Pochopien Ph.D., Donald J.  
REGISTRATION NUMBER: 32,167  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-707-8889  
TELEFAX: 312-707-9155  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2749 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single

TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Brassica napus  
STRAIN: oleifera  
INDIVIDUAL ISOLATE: W1  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: S-locus  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..2574  
PUBLICATION INFORMATION:  
AUTHORS: GORING, DAPHNE  
AUTHORS: ROTHSTEIN, STEVEN J.  
TITLE: THE S-LOCUS RECEPTOR KINASE GENE IN A  
TITLE: SELF-INCOMPATIBLE BRASSICA NAPUS LINE ENCODES A  
TITLE: FUNCTIONAL SERINE/THREONINE KINASE  
RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 2749  
US-08-265-628-1

Query Match 8 6%; Score 166.4; DB 1; Length 2749;  
Best Local Similarity 56.4%; Pred. No. 2.7e-34;  
Matches 352; Conservative 0; Mismatches 266; Indels 6; Gaps 2;

Qy 796 GAGGAGCTAGTAGAGCCCAATAGTTTCTCCGAGCGAAGTTGTAAGACAGCGCG 855  
Db 1558 GAAGCTGTGTGTAAGCCCAACCCAAATTTCTCAATGTATCAACATCGGACAGGTGT 1617  
Qy 856 TTGCTTACGTGCAAAAGGTGTGTTGCTTATGAGGAAAAGATTCTGTGAGCGTTG 915  
Db 1618 TTGCTTATTTGTTTCAAGGAGTAGATTACTGATGGCGAATAATGCGTAAAGGCTA 1677  
Qy 916 AAGGTTGGAGGTGTGAGGAGAGAGAGGAGTTTCAGGACAGGTTGATCATCAGCAGA 975  
Db 1678 TCAAAAACGTCGTTCAAGGAGCTGTGAGTTTATGATGAGTGAATGATCGGAGG 1737  
Qy 976 GTTCACCACAGGATCTGTGTCTTTGTTGTTATGATGCGCGGTGCCAAAAGATTG 1035  
Db 1738 CTTCAGATATTAACCTGTCCGAATTTCTGGCTGTGATGAGGACAGAGAGATG 1797  
Qy 1036 CTGTCTATGAGTTGTCTTACCAACATCTGAGGTTTCACTCCATG--CGAGGA 1092  
Db 1798 CTGTATATGAGTATTAAGAAATTTAAGCTTGATTTTATCTTTCGGAATTAACGA 1857  
Qy 1093 CGGCTACATGAGATGAGACCAAGATGAGATGCTCTGATCTGTAAGAGACTT 1152  
Db 1858 AGCTTACGTTAAATTTGAAGACAGATTCAACATTACCAATGTTGCTCCAGAGCTT 1917  
Qy 1153 TCTTATCTCATGAGATTGCAATCTTAAATCATTCACCGTGAATCAAGGCTTCAAC 1212  
Db 1918 TTAATCTTCAAGACTACAGGTTTATGATATCAACAGAGATATGAAGTATGATAC 1977  
Qy 1213 ATATTGATGATTTCAAGTTTGAAGCTAAGTTGCTATTTGCTTGTCAATAGTCT 1272  
Db 1978 ATTTGCTTATTAATAATATGACACCAAGATCTGGAATTTTGGATGGCCAGATCTT 2037  
Qy 1273 TCTGATCAAAACGAGATGATCAACAG--TGTGATGGAAACCTTGGTACTTGGCT 1329  
Db 2038 GCAAGGAGAGAGTGAAGCTAACAACAAGAGAGTGTGGAATCTTACGCTATCATGCT 2097  
Qy 1330 CCGGATACGCTGCAAGCGGAAAGCTCAAGGAGAGTGTGAGCTTTCTCATTTGGCGTT 1389  
Db 2098 CCGGAGTACGCAATGAGATGGGTATTTCTCGGAAAAATCAGATGTTTCAAGTTGAGTTC 2157  
Qy 1390 GTGCTTTTGAAGCTCATTAAGTGA 1413  
Db 2158 ATTGTTCTGAATATGTTAGTGA 2181

RESULT 14  
US-08-881-706-1

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; Sequence 1, Application US/08881706
; Patent No. 6245969
; GENERAL INFORMATION:
; APPLICANT: Chong, Joane
; APPLICANT: Li, Jiaming
; TITLE OF INVENTION: Receptor Kinase BIN1
; FILE REFERENCE: 07251/022001
; CURRENT APPLICATION NUMBER: US/08/881,706
; CURRENT FILING DATE: 1997-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4104
; TYPE: DNA
; ORGANISM: Arabidopsis sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (97) ..(3687)
US-08-881-706-1

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Query Match      8.4%; Score 162.4; DB 3; Length 4104;
Best Local Similarity 55.4%; Pred. No. 4e-33;
Matches 382; Conservative 0; Mismatches 296; Indels 12; Gaps 3;

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QY 788 TCACATACGAGAGGAGCTAGCTAGACCCACCAATGGTTTCCGAGCCGAACTTTAGGAC 847
DB 2708 TCACGTTTGGCGATCTTCTTCAAGCTACCAATGGTTCCATATGATGTCTGATTTGTT 2767
QY 848 AAGCGGGTTCGCTTACCTGACCAAAAGGTGTGCTTCTAGTGGGAAAGAGTGTCTGGA 907
DB 2768 CTGGTGGTTGGAGATTTTACAAAGCATTTTGAAGATGGAAGCCGGTGGCTATCA 2827
QY 908 AGCAGTTGAAAGTTGGAGTGTCAAGGAGAGAGAGAGGAGTTTCAGGACAGAGTTAGATCA 967
DB 2828 AGAACTGATTCATGTTTACCGGTCAAGGTGATAGAGATTCATGGCGGAGATGMAACA 2887
QY 968 TCACAGAGTTTACACACAGGAGCTGTGTCTCTTGTGTTTATTTGATCCCGGTGCA 1027
DB 2888 TTGGAGAGATCAAACTGAAATCTTGTCTCTTGTGTTTATTTGAAAGTTGGAGACG 2947
QY 1028 AAGATTGCTTGTCTATGAGTTTGTCTTAAACAATCTCGAGCTTCACTCCATGGC- 1086
DB 2948 AGCGGCTTCTTGAATGAGTTTGAAGTATGAAAGTTGAAGATTTTGAAGAC 3007
QY 1087 -----GAGGACGGCTTCAATGAAATGAGACACCAATGAAAGTTGCTTGGATCTG 1141
DB 3008 CCAAGAAAGGTGGGCTGAAACTTAATTTGCCACACGGCGGAGATTGGCATGATCAG 3067
QY 1142 CTAAAGGACTTCTTATCTTCAATGAGATTGCAATCTTAAATGATTTCACTGATATCA 1201
DB 3068 CTAAAGGCTTGTCTTCTTCAACCAATGAGATCCGCAATATCATCCAGAGACATGA 3127
QY 1202 AGGCTTCAACATATGATGATTTCAAGTTTGAAGTTGAAGTTGCTGATTTGGTCTG 1261
DB 3128 AATCCAGTAAATGCTTGTCTTGAAGATTTGGAAGCTCGGGTTTCAGATTTTGGCATGG 3187
QY 1262 CTAAAGTTGCTTCTGATACAAACGCAATGATCAACAGT--GTATGGGAACTTTG 1318
DB 3188 CGAGGCTGATGAGTGCATGATGATGATTTAAGCTCAGTATGATGCTGATCAACCGG 3247
QY 1319 GGTACTTGGCTCCGGAATAGCGTCAACGCGAAGCTCAGGAGAACTGACGTTTCT 1378
DB 3248 GTTACGTTCTTCAAGATATTTACCAAGTTTCAGGTCTTCAACAAAGAGACCTTATA 3307
QY 1379 CATTTGCGTTGCTTCTTGGAGCTCATTTACTGAGCTGACCCGTTGATGCCAATG 1438
DB 3308 GTTACGTTGCTTCTTACTGAGCTACTCAAGGCTTAAACGCGCAACGATTCACCGAT- 3366
QY 1439 TCTATGATGACAGCTTATGATGCTGG 1468
DB 3367 -TTTGAAGATTAACAACTTGTGATGG 3394

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RESULT 15
US-09-823-394-1
; Sequence 1, Application US/09823394
; Patent No. 6765085
; GENERAL INFORMATION:
; APPLICANT: Chory, Joane
; APPLICANT: Jiaming, Li
; TITLE OF INVENTION: Receptor Kinase, BIN 1
; FILE REFERENCE: SALKINS.012CP1
; CURRENT APPLICATION NUMBER: US/09/823,394
; CURRENT FILING DATE: 2001-03-30
; PRIOR FILING DATE: 1997-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 4104
; TYPE: DNA
; ORGANISM: Arabidopsis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (97) ... (3684)
US-09-823-394-1

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QY 848 AAGCGGGTTCGCTTACCTGACCAAAAGGTGTGCTTCTAGTGGGAAAGAGTGTCTGGA 907
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DB 3188 CGAGGCTGATGAGTGCATGATGATGATTTAAGCTCAGTATGATGCTGATCAACCGG 3247
QY 1319 GGTACTTGGCTCCGGAATAGCGTCAACGCGAAGCTCAGGAGAACTGACGTTTCT 1378
DB 3248 GTTACGTTCTTCAAGATATTTACCAAGTTTCAGGTCTTCAACAAAGAGACCTTATA 3307
QY 1379 CATTTGCGTTGCTTCTTGGAGCTCATTTACTGAGCTGACCCGTTGATGCCAATG 1438
DB 3308 GTTACGTTGCTTCTTACTGAGCTACTCAAGGCTTAAACGCGCAACGATTCACCGAT- 3366

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Qy	1439	TCTATGATGACAGCTTAGTTGACTGGG	1468
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Search completed: November 13, 2004, 10:58:32  
Job time : 126 secs



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: November 13, 2004, 12:25:15 ; Search time 122 Seconds

(without alignments)  
11326.013 Million cell updates/sec

Title: US-10-069-304-1  
Perfect score: 1944  
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Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 824507 seqs, 355394441 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

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	1	23	1.2	4626	1	US-08-306-691B-22	Sequence 22, App
	2	23	1.2	4626	5	PCT-US93-06251-27	Sequence 27, App
	3	20	1.0	609	4	US-09-800-729-55	Sequence 55, App
	4	20	1.0	852	4	US-09-252-991A-1274	Sequence 1274, App
	5	20	1.0	909	4	US-09-252-991A-1381	Sequence 1381, App
C	6	20	1.0	1092	4	US-09-252-991A-1287	Sequence 1287, App
	7	20	1.0	1680	4	US-09-248-796A-4378	Sequence 4378, App
	8	20	1.0	2838	4	US-09-248-796B-1640	Sequence 1640, App
	9	20	1.0	3097	3	US-09-228-986-11	Sequence 11, App
	10	20	1.0	3097	4	US-10-101-464A-11	Sequence 11, App
	11	20	1.0	5720	4	US-09-800-729-18	Sequence 18, App
C	12	20	1.0	41100	4	US-09-755-665-46	Sequence 16, App
	13	19	1.0	358	3	US-08-991-789A-168	Sequence 168, App
	14	19	1.0	358	3	US-09-062-451-168	Sequence 168, App
	15	19	1.0	358	4	US-09-598-326-168	Sequence 168, App
	16	19	1.0	358	4	US-09-289-198-168	Sequence 168, App
	17	19	1.0	358	4	US-09-429-755-168	Sequence 168, App
	18	19	1.0	402	4	US-09-248-796A-9061	Sequence 9061, App
	19	19	1.0	437	4	US-09-513-999C-2782	Sequence 2782, App
C	20	19	1.0	2487	4	US-09-187-330-4	Sequence 4, App
C	21	19	1.0	2487	4	US-09-187-330-54	Sequence 54, App
C	22	19	1.0	3621	4	US-09-635-872A-21	Sequence 21, App
C	23	19	1.0	3621	4	US-09-636-077A-21	Sequence 21, App
C	24	19	1.0	3621	4	US-09-636-060C-21	Sequence 21, App
C	25	19	1.0	3621	4	US-09-986-552-21	Sequence 21, App
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51	18	0.9	652	4	US-09-976-594-666	Sequence 666, App
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62	18	0.9	1390	4	US-09-270-767-13794	Sequence 13794, A
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104	18	0.9	12124	1	US-08-454-876-36	Sequence 36, Appl	177	17	0.9	855	2	US-08-924-759-15	Sequence 15, Appl
105	18	0.9	12124	2	US-08-457-364-36	Sequence 36, Appl	178	17	0.9	861	3	US-09-248-335-15	Sequence 46, Appl
106	18	0.9	12124	2	US-08-456-262-36	Sequence 36, Appl	179	17	0.9	870	4	US-09-792-024-46	Sequence 47, Ap
107	18	0.9	12124	2	US-08-456-240-36	Sequence 36, Appl	180	17	0.9	885	4	US-09-489-039A-4117	Sequence 4117, Ap
108	18	0.9	12124	2	US-08-455-736-36	Sequence 36, Appl	181	17	0.9	893	3	US-09-286-529-8	Sequence 8, Appl
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110	18	0.9	12124	3	US-09-350-600-36	Sequence 36, Appl	183	17	0.9	899	3	US-09-883-758-5	Sequence 10, Appl
111	18	0.9	12124	3	US-09-906-234-36	Sequence 36, Appl	184	17	0.9	914	4	US-08-935-450-10	Sequence 82, Appl
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113	18	0.9	1830121	4	US-09-557-884-31	Sequence 1, Appl	186	17	0.9	924	2	US-08-332-562A-82	Sequence 82, Appl
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120	17	0.9	51	4	US-09-443-199C-1152	Sequence 1152, Ap	193	17	0.9	1042	2	US-08-332-562A-131	Sequence 131, Ap
121	17	0.9	51	4	US-09-443-199C-1154	Sequence 1154, Ap	194	17	0.9	1050	3	US-09-199-637A-428	Sequence 428, Ap
122	17	0.9	51	4	US-09-443-199C-1155	Sequence 1155, Ap	195	17	0.9	1062	3	US-09-107-532A-1399	Sequence 1399, Ap
123	17	0.9	51	4	US-09-443-199C-1156	Sequence 1156, Ap	196	17	0.9	1107	4	US-09-252-991A-4828	Sequence 4828, Ap
124	17	0.9	51	4	US-09-443-199C-1157	Sequence 1157, Ap	197	17	0.9	1128	4	US-09-248-796A-4834	Sequence 4834, Ap
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136	17	0.9	142	4	US-09-513-999C-16239	Sequence 16239, A	209	17	0.9	1368	4	US-09-248-796A-2415	Sequence 2415, Ap
137	17	0.9	192	4	US-09-248-796A-7282	Sequence 7282, Ap	210	17	0.9	1366	4	US-09-489-039A-2452	Sequence 2452, Ap
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139	17	0.9	258	4	US-09-248-796A-7564	Sequence 7564, Ap	212	17	0.9	1444	4	US-09-614-221A-165	Sequence 15, Appl
140	17	0.9	285	4	US-09-513-999C-8469	Sequence 8469, Ap	213	17	0.9	1474	3	US-09-134-030-9	Sequence 9, Appl
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143	17	0.9	332	4	US-09-023-655-159	Sequence 159, Ap	216	17	0.9	1496	4	US-09-489-039A-1399	Sequence 1399, Ap
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163	17	0.9	645	4	US-09-134-000C-1423	Sequence 1423, Ap	236	17	0.9	1821	4	US-09-774-528-334	Sequence 334, Appl
164	17	0.9	687	4	US-09-252-991A-2936	Sequence 2936, Ap	237	17	0.9	1849	4	US-09-465-558-35	Sequence 35, Appl
165	17	0.9	692	4	US-09-270-767-7516	Sequence 7516, Ap	238	17	0.9	1951	4	US-09-227-357-45	Sequence 45, Appl
166	17	0.9	692	4	US-09-270-767-22798	Sequence 22798, A	239	17	0.9	2053	3	US-09-252-991A-3938	Sequence 3938, Ap
167	17	0.9	726	3	US-09-171-517B-3	Sequence 3, Appl	240	17	0.9	2061	4	US-08-154-915-5	Sequence 5, Appl
168	17	0.9	768	1	US-08-236-918A-5	Sequence 5, Appl	241	17	0.9	2100	1	US-10-101-464A-462	Sequence 462, Ap
169	17	0.9	768	3	US-09-150-864A-5	Sequence 5, Appl	242	17	0.9	2138	4	US-09-854-133-728	Sequence 728, Ap
170	17	0.9	773	1	US-09-328-475C-164	Sequence 164, Appl	243	17	0.9	2170	4	US-09-801-861-1	Sequence 1, Appl
171	17	0.9	800	1	US-08-390-858B-35	Sequence 35, Appl	244	17	0.9	2203	4	US-10-224-562-1	Sequence 1, Appl
172	17	0.9	803	1	US-08-390-858B-37	Sequence 37, Appl	245	17	0.9	2203	4	US-09-252-991A-3884	Sequence 3884, Ap
173	17	0.9	822	3	US-09-228-986-38	Sequence 38, Appl	246	17	0.9	2316	4		

C 247	17	0.9	2328	4	US-09-252-991A-3965	Sequence 3965, App	320	16	0.8	78	3	US-08-479-744A-36	Sequence 36, App1
C 248	17	0.9	2347	5	PCT-US96-03965-1	Sequence 1, App1	321	16	0.8	78	3	US-08-280-757B-36	Sequence 36, App1
C 249	17	0.9	2350	1	US-08-012-269A-1	Sequence 1, App1	322	16	0.8	78	4	US-09-227-595-5	Sequence 5, App1
C 250	17	0.9	2370	1	US-08-104-072B-7	Sequence 7, App1	323	16	0.8	78	4	US-09-425-762-36	Sequence 36, App1
C 251	17	0.9	2370	1	US-08-351-413-8	Sequence 8, App1	324	16	0.8	78	4	US-08-595-590B-5	Sequence 5, App1
C 252	17	0.9	2370	2	US-09-025-583-8	Sequence 8, App1	325	16	0.8	78	4	US-09-513-999C-31160	Sequence 31160, A
C 253	17	0.9	2372	4	US-09-023-655-1076	Sequence 1076, App	326	16	0.8	80	1	PCT-US91-03388-5	Sequence 5, App1
C 254	17	0.9	2457	4	US-09-919-497-42	Sequence 42, App1	327	16	0.8	80	1	US-07-800-364B-5	Sequence 5, App1
C 255	17	0.9	2508	4	US-09-489-039A-1569	Sequence 1569, App	328	16	0.8	86	1	US-08-150-331-47	Sequence 47, App1
C 256	17	0.9	2534	4	US-09-620-312D-80	Sequence 80, App1	329	16	0.8	86	1	US-08-569-284-47	Sequence 47, App1
C 257	17	0.9	2590	1	US-08-524-757-11	Sequence 11, App1	330	16	0.8	90	4	US-09-792-024-347	Sequence 347, App
C 258	17	0.9	2949	4	US-09-556-877-170	Sequence 170, App	331	16	0.8	103	4	US-09-513-999C-11666	Sequence 11666, A
C 259	17	0.9	2949	4	US-09-620-412C-170	Sequence 170, App	332	16	0.8	149	4	US-09-513-999C-32888	Sequence 32888, A
C 260	17	0.9	2949	4	US-09-598-419-170	Sequence 170, App	333	16	0.8	183	4	US-09-270-767-30393	Sequence 30393, A
C 261	17	0.9	3021	4	US-09-556-877-182	Sequence 182, App	334	16	0.8	186	4	US-09-248-796A-11344	Sequence 11344, A
C 262	17	0.9	3021	4	US-09-620-412C-182	Sequence 182, App	335	16	0.8	192	4	US-09-248-796A-5371	Sequence 5371, App
C 263	17	0.9	3021	4	US-09-598-419-182	Sequence 182, App	336	16	0.8	192	4	US-09-762-960-5	Sequence 5, App1
C 264	17	0.9	3045	4	US-09-596-248D-24	Sequence 24, App	337	16	0.8	192	4	US-09-248-796A-7100	Sequence 7100, App
C 265	17	0.9	3186	4	US-09-484-970B-168	Sequence 168, App	338	16	0.8	232	4	US-09-270-767-26013	Sequence 26013, App
C 266	17	0.9	3200	4	US-09-596-248D-46	Sequence 46, App	339	16	0.8	258	4	US-09-248-796A-1122	Sequence 1122, App
C 267	17	0.9	3255	4	US-09-016-434-1471	Sequence 1471, App	340	16	0.8	261	4	US-09-248-796A-11344	Sequence 11344, App
C 268	17	0.9	3324	4	US-09-612-402B-24	Sequence 24, App1	341	16	0.8	270	4	US-09-513-999C-14881	Sequence 14881, A
C 269	17	0.9	3331	3	US-08-864-038A-2	Sequence 2, App1	342	16	0.8	271	3	US-09-328-111-632	Sequence 632, App
C 270	17	0.9	3331	3	US-08-864-038A-4	Sequence 4, App1	343	16	0.8	273	3	US-09-248-796A-13017	Sequence 13017, A
C 271	17	0.9	3354	4	US-09-612-402B-23	Sequence 23, App1	344	16	0.8	283	3	US-09-172-711-25	Sequence 25, App1
C 272	17	0.9	3388	1	US-08-197-792-32	Sequence 32, App1	345	16	0.8	288	4	US-09-621-976-10038	Sequence 10038, A
C 273	17	0.9	3588	1	US-08-459-850-32	Sequence 32, App1	346	16	0.8	292	4	US-09-621-976-10076	Sequence 10076, A
C 274	17	0.9	3588	1	US-08-459-214-32	Sequence 32, App1	347	16	0.8	293	4	US-09-313-294A-958	Sequence 958, App
C 275	17	0.9	3588	1	US-08-459-214-32	Sequence 32, App1	348	16	0.8	293	4	US-09-313-294A-958	Sequence 958, App
C 276	17	0.9	3660	4	US-09-517-467B-3	Sequence 3, App1	349	16	0.8	297	4	US-09-016-434-1032	Sequence 1032, App
C 277	17	0.9	3728	1	US-08-111-939-1	Sequence 1, App1	350	16	0.8	303	4	US-09-313-294A-945	Sequence 945, App
C 278	17	0.9	3747	1	US-08-044-618-5	Sequence 5, App1	351	16	0.8	303	4	US-09-248-796A-7417	Sequence 7417, App
C 279	17	0.9	3792	3	US-08-860-886-1	Sequence 1, App1	352	16	0.8	309	4	US-09-313-294A-4076	Sequence 4076, App
C 280	17	0.9	3852	4	US-09-245-248B-29	Sequence 29, App1	353	16	0.8	309	4	US-09-513-999C-26869	Sequence 26869, A
C 281	17	0.9	3887	4	US-09-976-594-660	Sequence 660, App	354	16	0.8	311	4	US-09-513-999C-27757	Sequence 27757, A
C 282	17	0.9	3991	3	US-08-506-296B-3	Sequence 3, App1	355	16	0.8	311	4	US-09-313-294A-7021	Sequence 7021, App
C 283	17	0.9	4059	2	US-08-485-139-1	Sequence 1, App1	356	16	0.8	315	4	US-09-248-796A-12307	Sequence 12307, A
C 284	17	0.9	4059	3	US-08-750-357-1	Sequence 1, App1	357	16	0.8	320	4	US-09-270-767-29475	Sequence 29475, A
C 285	17	0.9	4133	4	US-09-688-188B-11	Sequence 11, App1	358	16	0.8	322	4	US-09-621-976-16469	Sequence 16469, A
C 286	17	0.9	4133	4	US-09-291-417D-11	Sequence 11, App1	359	16	0.8	328	4	US-09-270-767-8036	Sequence 8036, App
C 287	17	0.9	4218	4	US-09-081-385-8	Sequence 8, App1	360	16	0.8	328	4	US-09-270-767-23318	Sequence 23318, A
C 288	17	0.9	4418	4	US-09-976-594-773	Sequence 773, App	361	16	0.8	331	4	US-09-462-917A-51	Sequence 51, App1
C 289	17	0.9	4432	4	US-09-774-528-148	Sequence 148, App	362	16	0.8	333	4	US-09-621-976-18183	Sequence 18183, A
C 290	17	0.9	4432	4	US-09-612-402B-1	Sequence 1, App1	363	16	0.8	336	4	US-09-248-796A-7944	Sequence 7944, App
C 291	17	0.9	4453	1	US-08-770-761A-6	Sequence 4, App1	364	16	0.8	339	4	US-09-621-976-1333	Sequence 1333, App
C 292	17	0.9	4540	1	US-08-770-761A-6	Sequence 6, App1	365	16	0.8	351	4	US-09-248-796A-10722	Sequence 10722, A
C 293	17	0.9	4621	1	US-08-770-761A-1	Sequence 1, App1	366	16	0.8	352	4	US-09-513-999C-11862	Sequence 11862, A
C 294	17	0.9	4824	2	US-08-485-139-5	Sequence 5, App1	367	16	0.8	360	4	US-10-101-464A-395	Sequence 395, App
C 295	17	0.9	5257	3	US-08-750-357-5	Sequence 5, App1	368	16	0.8	362	4	US-09-513-999C-3622	Sequence 3622, App
C 296	17	0.9	5257	3	US-09-917-254-47	Sequence 47, App1	369	16	0.8	368	4	US-09-621-976-18182	Sequence 18182, A
C 297	17	0.9	5962	1	US-08-188-582-10	Sequence 10, App1	370	16	0.8	370	4	US-09-710-279-245	Sequence 245, App
C 298	17	0.9	6223	4	US-08-646-715-10	Sequence 10, App1	371	16	0.8	370	4	US-09-270-767-8290	Sequence 8290, App
C 299	17	0.9	6304	4	US-09-620-312D-459	Sequence 459, App	372	16	0.8	370	4	US-09-270-767-23572	Sequence 23572, A
C 300	17	0.9	6382	4	US-09-620-312D-460	Sequence 460, App	373	16	0.8	373	4	US-09-270-767-28792	Sequence 28792, A
C 301	17	0.9	6382	4	US-09-620-312D-460	Sequence 460, App	374	16	0.8	378	3	US-09-710-279-3015	Sequence 3015, App
C 302	17	0.9	14736	4	US-08-961-527-171	Sequence 171, App	375	16	0.8	378	3	US-08-513-974B-33	Sequence 33, App1
C 303	17	0.9	15936	4	US-09-147-119-1	Sequence 1, App1	376	16	0.8	378	3	US-08-776-971-28	Sequence 28, App1
C 304	17	0.9	24979	2	US-08-147-777-3	Sequence 3, App1	377	16	0.8	378	4	US-09-461-436B-33	Sequence 33, App1
C 305	17	0.9	24979	5	US-08-452-872-3	Sequence 3, App1	378	16	0.8	378	4	US-09-576-2296-28	Sequence 28, App1
C 306	17	0.9	24979	5	PCT-US93-03985-3	Sequence 3, App1	379	16	0.8	381	4	US-09-270-767-7989	Sequence 7989, App
C 307	17	0.9	32155	4	US-08-311-731A-1	Sequence 1, App1	380	16	0.8	382	4	US-09-270-767-23271	Sequence 23271, A
C 308	17	0.9	42235	3	US-09-199-637A-1	Sequence 1, App1	381	16	0.8	406	4	US-09-513-999C-11347	Sequence 11347, A
C 309	17	0.9	44377	2	US-08-804-227C-7	Sequence 7, App1	382	16	0.8	412	4	US-08-899-786-24	Sequence 24, App1
C 310	17	0.9	48763	4	US-08-804-198-1	Sequence 1, App1	383	16	0.8	426	4	US-09-513-999C-11346	Sequence 11346, A
C 311	17	0.9	48763	4	US-09-916-204-3	Sequence 3, App1	384	16	0.8	434	3	US-09-621-976-11124	Sequence 11124, A
C 312	17	0.9	87350	3	US-10-282-048-3	Sequence 3, App1	385	16	0.8	434	3	US-09-621-976-11124	Sequence 11124, A
C 313	17	0.9	87350	3	US-08-781-891-79	Sequence 79, App1	386	16	0.8	440	4	US-08-513-974B-165	Sequence 165, App
C 314	17	0.9	87350	4	US-09-618-166-79	Sequence 79, App1	387	16	0.8	440	4	US-08-776-971-105	Sequence 105, App
C 315	17	0.9	87543	4	US-09-791-211-3	Sequence 3, App1	388	16	0.8	444	4	US-09-270-767-1375	Sequence 1375, App
C 316	17	0.9	114793	4	US-10-148-806-3	Sequence 3, App1	389	16	0.8	444	4	US-09-270-767-16657	Sequence 16657, A
C 317	17	0.9	4403765	3	US-09-103-840A-2	Sequence 2, App1	390	16	0.8	444	4	US-09-621-976-962	Sequence 962, App
C 318	17	0.9	441529	3	US-09-103-840A-2	Sequence 1, App1	391	16	0.8	446	4	US-09-248-796A-5986	Sequence 5986, App
C 319	16	0.8	20	4	US-09-596-248D-32	Sequence 32, App1	392	16	0.8	446	4	US-09-641-638-500	Sequence 500, App
C 320	16	0.8	20	4	US-09-596-248D-33	Sequence 33, App1	393	16	0.8	446	4	US-10-170-097-500	Sequence 500, App

C 393	16	0.8	447	4	US-09-621-976-17257	Sequence 17257, A	466	16	0.8	838	4	US-08-781-986A-827	Sequence 827, App
C 394	16	0.8	448	4	US-09-270-767-4398	Sequence 4398, App	467	16	0.8	842	3	US-08-952-796-1	Sequence 1, Appli
C 395	16	0.8	448	4	US-09-270-767-19680	Sequence 19680, A	468	16	0.8	842	3	US-08-940-136-259	Sequence 259, App
C 396	16	0.8	450	2	US-08-966-316-5	Sequence 5, Appli	C 469	16	0.8	855	4	US-09-248-796A-1869	Sequence 1869, App
C 397	16	0.8	456	4	US-09-513-999C-11345	Sequence 11345, A	470	16	0.8	857	4	US-09-270-767-28454	Sequence 28454, A
C 398	16	0.8	462	4	US-09-401-064-165	Sequence 165, App	471	16	0.8	857	4	US-09-919-039-248	Sequence 248, App
C 399	16	0.8	470	3	US-09-168-930-224	Sequence 224, App	C 472	16	0.8	858	4	US-09-482-273-46	Sequence 46, Appli
C 400	16	0.8	470	3	US-09-312-283C-224	Sequence 224, App	473	16	0.8	863	1	US-08-448-606-7	Sequence 7, Appli
C 401	16	0.8	472	4	US-09-621-976-18485	Sequence 18485, A	474	16	0.8	870	4	US-09-248-796A-4317	Sequence 4317, App
C 402	16	0.8	473	4	US-09-621-976-374	Sequence 374, App	475	16	0.8	873	4	US-09-023-655-83	Sequence 383, App
C 403	16	0.8	477	4	US-09-583-110-886	Sequence 886, App	C 476	16	0.8	873	4	US-09-248-796A-6838	Sequence 6838, App
C 404	16	0.8	481	4	US-09-644-907B-5	Sequence 5, Appli	C 477	16	0.8	879	4	US-08-513-999C-1806	Sequence 1806, App
C 405	16	0.8	485	4	US-09-686-583B-34	Sequence 34, Appli	C 478	16	0.8	900	1	US-08-480-481-6	Sequence 6, Appli
C 406	16	0.8	486	4	US-09-513-999C-11348	Sequence 11348, A	C 479	16	0.8	900	4	US-09-252-991A-1626	Sequence 1626, App
C 407	16	0.8	488	4	US-09-270-767-10584	Sequence 10584, A	C 480	16	0.8	921	4	US-09-107-532A-839	Sequence 839, App
C 408	16	0.8	496	4	US-09-621-976-1717	Sequence 1717, App	481	16	0.8	922	4	US-09-620-312D-1031	Sequence 1031, App
C 409	16	0.8	497	4	US-09-621-976-15691	Sequence 15691, A	482	16	0.8	924	3	US-08-983-409-3	Sequence 3, Appli
C 410	16	0.8	498	4	US-09-270-767-7392	Sequence 7392, App	C 483	16	0.8	924	3	US-09-107-532A-2518	Sequence 2518, App
C 411	16	0.8	498	4	US-09-270-767-22674	Sequence 22674, A	C 484	16	0.8	929	4	US-09-513-999C-14935	Sequence 14935, A
C 412	16	0.8	507	4	US-09-762-960-11	Sequence 11, Appli	485	16	0.8	935	4	US-09-919-039-26	Sequence 26, Appli
C 413	16	0.8	543	4	US-09-252-991A-11918	Sequence 11918, A	C 486	16	0.8	958	2	US-08-757-046A-5	Sequence 5, Appli
C 414	16	0.8	543	4	US-09-270-767-1945	Sequence 1945, App	C 487	16	0.8	958	3	US-09-447-208-5	Sequence 5, Appli
C 415	16	0.8	543	4	US-09-270-767-17227	Sequence 17227, A	C 488	16	0.8	958	3	US-09-135-988-5	Sequence 5, Appli
C 416	16	0.8	546	4	US-09-270-767-531	Sequence 531, App	C 489	16	0.8	958	3	US-09-277-716-5	Sequence 5, Appli
C 417	16	0.8	546	4	US-09-799-451-89	Sequence 1813, A	C 490	16	0.8	958	3	US-08-597-274A-5	Sequence 5, Appli
C 418	16	0.8	546	4	US-09-686-583B-35	Sequence 89, Appli	C 491	16	0.8	958	4	US-09-908-909-5	Sequence 5, Appli
C 419	16	0.8	550	4	US-09-686-583B-35	Sequence 35, Appli	C 492	16	0.8	958	4	US-09-609-161B-5	Sequence 5, Appli
C 420	16	0.8	561	4	US-09-248-796A-1741	Sequence 1741, App	C 493	16	0.8	958	4	US-08-990-103-5	Sequence 5, Appli
C 421	16	0.8	582	4	US-09-793-024-41	Sequence 41, Appli	C 494	16	0.8	958	4	US-09-746-485A-5	Sequence 5, Appli
C 422	16	0.8	603	3	US-08-952-786-14	Sequence 14, Appli	C 495	16	0.8	958	4	US-10-126-139-5	Sequence 5, Appli
C 423	16	0.8	606	4	US-09-621-976-16568	Sequence 16568, A	C 496	16	0.8	958	4	US-10-126-798-5	Sequence 5, Appli
C 424	16	0.8	609	1	US-07-834-902-2	Sequence 2, Appli	C 497	16	0.8	958	4	US-10-126-777-5	Sequence 5, Appli
C 425	16	0.8	609	1	US-08-018-994-2	Sequence 2, Appli	498	16	0.8	964	1	US-08-448-606-5	Sequence 5, Appli
C 426	16	0.8	609	1	US-08-294-675A-2	Sequence 2, Appli	C 499	16	0.8	966	4	US-09-489-039A-1797	Sequence 1797, App
C 427	16	0.8	609	5	PCT-US94-00928-1	Sequence 1, Appli	C 500	16	0.8	975	4	US-09-489-039A-632	Sequence 632, App
C 428	16	0.8	615	4	US-09-513-999C-730	Sequence 730, App	C 501	16	0.8	1000	4	US-09-023-655-1428	Sequence 1428, App
C 429	16	0.8	615	4	US-09-385-982-238	Sequence 238, App	C 502	16	0.8	1002	4	US-09-248-796A-5029	Sequence 5029, App
C 430	16	0.8	618	4	US-09-710-279-2183	Sequence 2183, App	C 503	16	0.8	1021	4	US-09-177-650-127	Sequence 127, App
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C 432	16	0.8	633	4	US-09-248-796A-1367	Sequence 1367, App	C 505	16	0.8	1044	4	US-09-710-279-1267	Sequence 1267, App
C 433	16	0.8	633	4	US-09-248-796A-11732	Sequence 11732, A	C 506	16	0.8	1050	1	US-08-480-481-3	Sequence 3, Appli
C 434	16	0.8	640	4	US-09-270-767-1309	Sequence 1309, App	C 507	16	0.8	1050	1	US-08-480-481-4	Sequence 4, Appli
C 435	16	0.8	640	4	US-09-270-767-16591	Sequence 16591, A	C 508	16	0.8	1056	4	US-09-134-001C-2655	Sequence 2655, App
C 436	16	0.8	651	4	US-09-187-999-20	Sequence 20, Appli	C 509	16	0.8	1060	4	US-09-023-655-557	Sequence 557, App
C 437	16	0.8	657	4	US-09-248-796A-320	Sequence 320, App	C 510	16	0.8	1062	4	US-09-668-680-10	Sequence 10, Appli
C 438	16	0.8	662	3	US-08-927-219-42	Sequence 42, Appli	C 511	16	0.8	1113	3	US-09-172-353-1	Sequence 1, Appli
C 439	16	0.8	670	4	US-09-513-999C-14968	Sequence 14968, A	C 512	16	0.8	1113	4	US-09-976-594-411	Sequence 411, App
C 440	16	0.8	678	4	US-08-956-171E-792	Sequence 792, App	C 513	16	0.8	1123	4	US-08-983-409-5	Sequence 5, Appli
C 441	16	0.8	678	4	US-08-781-986A-792	Sequence 792, App	C 514	16	0.8	1133	3	US-09-983-409-5	Sequence 5, Appli
C 442	16	0.8	689	4	US-09-513-999C-14965	Sequence 14965, A	C 515	16	0.8	1146	4	US-09-248-796A-6764	Sequence 6764, App
C 443	16	0.8	690	4	US-09-248-796A-4601	Sequence 4601, App	C 516	16	0.8	1149	3	US-09-422-487-6	Sequence 6, Appli
C 444	16	0.8	693	4	US-10-140-002-499	Sequence 499, App	C 517	16	0.8	1149	3	US-09-378-088A-128	Sequence 128, App
C 445	16	0.8	699	2	US-08-756-387B-7	Sequence 7, Appli	C 518	16	0.8	1149	3	US-09-643-5968A-128	Sequence 128, App
C 446	16	0.8	699	3	US-09-285-873-7	Sequence 7, Appli	C 519	16	0.8	1152	2	US-08-933-750C-81	Sequence 81, Appli
C 447	16	0.8	699	4	US-09-944-277A-7	Sequence 7, Appli	C 520	16	0.8	1152	3	US-09-234-613-81	Sequence 81, Appli
C 448	16	0.8	707	3	US-08-998-416-729	Sequence 729, App	C 521	16	0.8	1155	4	US-09-248-796A-5987	Sequence 5987, App
C 449	16	0.8	707	3	US-08-998-416-940	Sequence 940, App	C 522	16	0.8	1155	4	US-09-248-796A-9481	Sequence 9481, App
C 450	16	0.8	711	3	US-09-134-001C-1248	Sequence 1248, App	C 523	16	0.8	1158	4	US-09-248-796A-4348	Sequence 4348, App
C 451	16	0.8	729	4	US-09-107-532A-120	Sequence 120, App	C 524	16	0.8	1161	4	US-09-686-583B-47	Sequence 47, Appli
C 452	16	0.8	744	4	US-09-513-999C-14957	Sequence 14957, A	C 525	16	0.8	1161	4	US-09-686-583B-49	Sequence 49, Appli
C 453	16	0.8	744	4	US-09-328-352-531	Sequence 531, App	C 526	16	0.8	1168	4	US-09-270-767-662	Sequence 662, App
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C 455	16	0.8	774	2	US-08-756-387B-4	Sequence 4, Appli	C 528	16	0.8	1174	1	US-07-865-933-10	Sequence 10, Appli
C 456	16	0.8	774	3	US-08-756-387B-5	Sequence 5, Appli	C 529	16	0.8	1174	4	US-09-103-663-10	Sequence 10, Appli
C 457	16	0.8	774	3	US-09-285-873-4	Sequence 4, Appli	C 530	16	0.8	1174	4	US-09-270-767-27834	Sequence 27834, A
C 458	16	0.8	774	3	US-09-285-873-5	Sequence 5, Appli	C 531	16	0.8	1181	2	US-08-632-598-2	Sequence 2, Appli
C 459	16	0.8	774	4	US-09-944-277A-4	Sequence 4, Appli	C 532	16	0.8	1181	3	US-09-221-240-2	Sequence 2, Appli
C 460	16	0.8	774	4	US-09-944-277A-5	Sequence 5, Appli	C 533	16	0.8	1181	3	US-09-149-476-310	Sequence 310, App
C 461	16	0.8	801	1	US-07-959-946-4	Sequence 4, Appli	C 534	16	0.8	1191	3	US-09-046-992-3	Sequence 3, Appli
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C 463	16	0.8	801	5	PCT-US92-08634-4	Sequence 4, Appli	C 536	16	0.8	1191	4	US-09-686-583B-46	Sequence 46, Appli
C 464	16	0.8	810	3	US-08-213-419B-12	Sequence 12, Appli	C 537	16	0.8	1198	2	US-08-756-387B-1	Sequence 1, Appli
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543	16	0.8	1203	3	US-09-086-010-1	Sequence 1, Appli	616	16	0.8	1881	4	US-09-556-916-21	Sequence 21, Appli
544	16	0.8	1212	4	US-09-149-476-186	Sequence 186, App	617	16	0.8	1884	4	US-09-556-916-1	Sequence 1, Appli
545	16	0.8	1212	4	US-09-710-279-1521	Sequence 1521, Ap	618	16	0.8	1884	4	US-09-556-916-3	Sequence 3, Appli
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547	16	0.8	1239	4	US-09-248-796A-10434	Sequence 10434, A	620	16	0.8	1884	4	US-09-556-916-9	Sequence 9, Appli
548	16	0.8	1242	4	US-09-016-433-1283	Sequence 1283, Ap	621	16	0.8	1884	4	US-09-556-916-11	Sequence 11, Appli
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554	16	0.8	1296	4	US-09-894-844-47	Sequence 14261, A	627	16	0.8	1926	1	US-08-278-722A-22	Sequence 26, Appli
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565	16	0.8	1463	4	US-09-270-767-8265	Sequence 8265, Ap	638	16	0.8	1926	2	US-08-445-468A-22	Sequence 22, Appli
566	16	0.8	1479	2	US-08-199-485-1	Sequence 23517, A	639	16	0.8	1926	2	US-08-901-200A-9	Sequence 9, Appli
567	16	0.8	1482	1	US-09-252-991A-11453	Sequence 11453, A	640	16	0.8	1926	2	US-08-449-700-26	Sequence 26, Appli
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576	16	0.8	1530	4	US-09-248-796A-2825	Sequence 107, App	649	16	0.8	1926	3	US-09-170-936-22	Sequence 9, Appli
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582	16	0.8	1569	2	US-08-559-221-1	Sequence 1, Appli	655	16	0.8	1926	5	US-08-957-425-26	Sequence 26, Appli
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587	16	0.8	1644	4	US-09-270-767-16902	Sequence 16902, A	660	16	0.8	1926	5	PCT-US93-07231-22	Sequence 22, Appli
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596	16	0.8	1725	4	US-09-634-238-130	Sequence 130, App	669	16	0.8	1935	4	US-09-636-215-817	Sequence 817, App
597	16	0.8	1743	4	US-09-556-916-17	Sequence 17, Appli	670	16	0.8	1935	4	US-09-685-166A-817	Sequence 817, App
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608	16	0.8	1832	4	US-09-686-583B-44	Sequence 44, Appli	681	16	0.8	2003	4	US-09-894-698-3	Sequence 3, Appli
609	16	0.8	1836	4	US-09-248-796A-10454	Sequence 10454, A	682	16	0.8	2051	1	US-08-343-785-7	Sequence 7, Appli
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611	16	0.8	1842	4	US-09-248-796A-2421	Sequence 2421, Ap	684	16	0.8	2051	3	US-08-946-458-7	Sequence 7, Appli

C 685	16	0.8	2070	4	US-09-107-532A-1284	Sequence 1284, Ap	758	16	0.8	3516	4	US-09-710-279-3852	Sequence 3852, Ap
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C 697	16	0.8	2253	4	US-10-314-881-8	Sequence 8, Appli	C 770	16	0.8	3923	2	US-08-129-485-2	Sequence 2, Appli
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C 703	16	0.8	2306	6	5198359-3	Sequence 5198359-3	C 776	16	0.8	4458	4	US-10-370-659-1	Sequence 1, Appli
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C 706	16	0.8	2310	4	US-09-919-039-249	Sequence 249, App	C 779	16	0.8	4481	4	US-09-707-919A-20	Sequence 20, Appli
C 707	16	0.8	2329	3	US-08-956-322-1	Sequence 1, Appli	C 780	16	0.8	4481	4	US-09-083-268-2	Sequence 2, Appli
C 708	16	0.8	2352	4	US-09-533-029-117	Sequence 117, App	C 781	16	0.8	4512	4	US-09-792-616-2	Sequence 2, Appli
C 709	16	0.8	2352	4	US-09-724-586A-2	Sequence 2, Appli	C 782	16	0.8	4612	4	US-09-626-301-1	Sequence 1, Appli
C 710	16	0.8	2352	4	US-09-600-823-2	Sequence 2, Appli	C 783	16	0.8	4642	4	US-09-566-921-4	Sequence 4, Appli
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C 712	16	0.8	2370	1	US-08-351-413-8	Sequence 8, Appli	C 785	16	0.8	4739	3	US-08-685-871-1	Sequence 1, Appli
C 713	16	0.8	2370	2	US-09-025-583-8	Sequence 8, Appli	C 786	16	0.8	4853	3	US-08-881-450A-22	Sequence 22, Appli
C 714	16	0.8	2417	4	US-09-216-333B-306	Sequence 306, App	C 787	16	0.8	4890	4	US-09-677-046A-3	Sequence 3, Appli
C 715	16	0.8	2417	4	US-09-216-333B-308	Sequence 308, App	C 788	16	0.8	4943	4	US-09-677-046A-7	Sequence 7, Appli
C 716	16	0.8	2433	4	US-08-999-689A-2	Sequence 2, Appli	C 789	16	0.8	4970	4	US-09-816-095-1	Sequence 1, Appli
C 717	16	0.8	2433	4	US-09-944-807-3	Sequence 3, Appli	C 790	16	0.8	5000	4	US-08-956-171E-241	Sequence 241, App
C 718	16	0.8	2480	4	US-09-799-451-87	Sequence 87, Appli	C 791	16	0.8	5000	4	US-08-781-986A-241	Sequence 241, App
C 719	16	0.8	2493	4	US-09-252-991A-11987	Sequence 11987, A	C 792	16	0.8	5133	5	PCT-US96-01314-339	Sequence 39, Appli
C 720	16	0.8	2556	4	US-09-817-310-1	Sequence 1, Appli	C 793	16	0.8	5137	5	US-08-476-062A-39	Sequence 39, Appli
C 721	16	0.8	2560	3	US-09-305-640-1	Sequence 1, Appli	C 794	16	0.8	5138	2	US-09-677-046A-5	Sequence 5, Appli
C 722	16	0.8	2565	4	US-09-105-058C-26	Sequence 26, Appli	C 795	16	0.8	5170	4	US-08-688-376-1	Sequence 1, Appli
C 723	16	0.8	2571	4	US-09-248-796A-1986	Sequence 1986, Ap	C 796	16	0.8	5394	3	US-08-688-376-1	Sequence 1, Appli
C 724	16	0.8	2748	4	US-09-270-767-13675	Sequence 13675, A	C 797	16	0.8	5614	4	US-08-956-171E-99	Sequence 99, Appli
C 725	16	0.8	2797	4	US-09-799-451-563	Sequence 563, App	C 798	16	0.8	5614	4	US-08-781-986A-99	Sequence 99, Appli
C 726	16	0.8	2823	4	US-09-704-611-4	Sequence 4, Appli	C 799	16	0.8	5668	3	US-09-112-096-14	Sequence 14, Appli
C 727	16	0.8	2868	4	US-10-140-002-119	Sequence 119, App	C 800	16	0.8	5668	4	US-09-636-215-777	Sequence 777, App
C 728	16	0.8	2886	4	US-09-221-017B-863	Sequence 863, App	C 801	16	0.8	5668	4	US-09-685-166A-777	Sequence 777, App
C 729	16	0.8	2892	4	US-09-704-611-3	Sequence 3, Appli	C 802	16	0.8	5668	4	US-09-679-426-777	Sequence 777, App
C 730	16	0.8	2914	4	US-09-177-650-6	Sequence 6, Appli	C 803	16	0.8	5682	4	US-10-164-595-1	Sequence 1, Appli
C 731	16	0.8	2991	4	US-09-252-991A-12025	Sequence 12025, A	C 804	16	0.8	5926	4	US-09-917-254-41	Sequence 41, Appli
C 732	16	0.8	3014	1	US-08-628-939-1	Sequence 1, Appli	C 805	16	0.8	6203	3	US-09-134-218-3	Sequence 3, Appli
C 733	16	0.8	3014	1	US-08-759-873-1	Sequence 1, Appli	C 806	16	0.8	7060	4	US-09-221-017B-479	Sequence 479, App
C 734	16	0.8	3014	4	US-09-016-434-1244	Sequence 1244, Ap	C 807	16	0.8	7063	4	US-09-485-632B-5	Sequence 5, Appli
C 735	16	0.8	3105	3	US-08-542-635-1	Sequence 1, Appli	C 808	16	0.8	7445	3	US-09-178-973B-8	Sequence 8, Appli
C 736	16	0.8	3109	4	US-08-938-291A-1	Sequence 1, Appli	C 809	16	0.8	7445	3	US-09-419-568F-8	Sequence 8, Appli
C 737	16	0.8	3109	4	US-09-589-619-1	Sequence 1, Appli	C 810	16	0.8	7445	3	US-09-354-243B-8	Sequence 8, Appli
C 738	16	0.8	3153	4	US-09-710-279-3348	Sequence 3348, Ap	C 811	16	0.8	7481	4	US-08-956-171E-236	Sequence 236, App
C 739	16	0.8	3161	4	US-09-799-451-385	Sequence 385, App	C 812	16	0.8	7680	3	US-08-781-986A-236	Sequence 236, App
C 740	16	0.8	3209	4	US-09-976-594-671	Sequence 671, App	C 813	16	0.8	7680	3	US-09-210-748A-3	Sequence 3, Appli
C 741	16	0.8	3228	4	US-09-799-451-752	Sequence 752, App	C 814	16	0.8	7680	4	US-09-939-581A-3	Sequence 3, Appli
C 742	16	0.8	3245	4	US-09-774-528-352	Sequence 352, App	C 815	16	0.8	7812	4	US-09-485-632B-9	Sequence 9, Appli
C 743	16	0.8	3248	4	US-09-976-594-418	Sequence 418, App	C 816	16	0.8	8146	4	US-09-976-594-725	Sequence 725, App
C 744	16	0.8	3251	3	US-09-085-199B-5	Sequence 6, Appli	C 817	16	0.8	8146	4	US-09-976-594-725	Sequence 725, App
C 745	16	0.8	3263	3	US-09-710-279-3595	Sequence 3595, Ap	C 818	16	0.8	9416	4	US-08-823-895A-26	Sequence 26, Appli
C 746	16	0.8	3267	4	US-09-710-279-4042	Sequence 4042, Ap	C 819	16	0.8	9416	4	US-10-104-966-13	Sequence 13, Appli
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C 749	16	0.8	3282	4	US-09-919-039-274	Sequence 274, App	C 822	16	0.8	10034	3	US-09-771-357-102	Sequence 103, App
C 750	16	0.8	3332	4	US-09-710-279-3928	Sequence 3928, App	C 823	16	0.8	10660	2	US-08-267-803B-8	Sequence 8, Appli
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C 757	16	0.8	3465	3	US-08-914-999-5	Sequence 5, Appli	C 830	16	0.8	11917	4	US-09-566-921-32	Sequence 32, Appli



C 831	16	0.8	11917	4	US-09-566-921-32	Sequence 32, Appl	C 904	15	0.8	54	2	US-08-541-780-44	Sequence 44, Appl
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C 833	16	0.8	12732	4	US-09-670-314-1	Sequence 1, Appl	C 906	15	0.8	63	6	5498600-29	Patent No. 5498600
C 834	16	0.8	13542	4	US-08-956-171E-154	Sequence 154, App	C 907	15	0.8	80	1	US-08-425-335-119	Sequence 119, App
C 835	16	0.8	13542	4	US-08-781-986A-154	Sequence 154, App	C 908	15	0.8	80	1	US-08-488-113B-119	Sequence 119, App
C 836	16	0.8	13842	3	US-09-105-537-30	Sequence 30, Appl	C 909	15	0.8	80	1	US-08-488-113B-141	Sequence 141, App
C 837	16	0.8	13865	3	US-09-009-217-11	Sequence 11, Appl	C 910	15	0.8	80	1	US-08-477-484B-119	Sequence 119, App
C 838	16	0.8	13865	3	US-09-009-656-11	Sequence 11, Appl	C 911	15	0.8	80	1	US-08-477-484B-141	Sequence 141, App
C 839	16	0.8	13865	3	US-09-054-272-11	Sequence 11, Appl	C 912	15	0.8	80	1	US-08-107-669D-131	Sequence 31, Appl
C 840	16	0.8	15872	3	US-09-105-537-1	Sequence 1, Appl	C 913	15	0.8	80	1	US-08-107-669D-62	Sequence 62, Appl
C 841	16	0.8	15872	4	US-09-091-609-3	Sequence 3, Appl	C 914	15	0.8	80	1	US-08-472-788A-31	Sequence 31, Appl
C 842	16	0.8	15872	4	US-09-091-609-3	Sequence 3, Appl	C 915	15	0.8	80	1	US-08-472-788A-51	Sequence 51, Appl
C 843	16	0.8	18853	4	US-09-820-005-3	Sequence 3, Appl	C 916	15	0.8	80	1	US-08-472-788A-62	Sequence 62, Appl
C 844	16	0.8	18853	4	US-10-109-855-3	Sequence 3, Appl	C 917	15	0.8	80	1	US-08-477-531B-11	Sequence 11, Appl
C 845	16	0.8	19390	4	US-08-961-527-86	Sequence 86, Appl	C 918	15	0.8	80	1	US-08-477-531B-62	Sequence 62, Appl
C 846	16	0.8	19390	4	US-08-961-527-86	Sequence 86, Appl	C 919	15	0.8	80	2	US-08-646-360-119	Sequence 119, App
C 847	16	0.8	22067	3	US-08-961-527-99	Sequence 99, Appl	C 920	15	0.8	80	2	US-08-646-360-170	Sequence 170, App
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C 849	16	0.8	31960	3	US-09-453-702B-11	Sequence 5, Appl	C 922	15	0.8	80	2	US-08-646-360-170	Sequence 170, App
C 850	16	0.8	36741	3	US-09-301-665-3	Sequence 11, Appl	C 923	15	0.8	80	2	US-08-646-360-170	Sequence 170, App
C 851	16	0.8	36741	3	US-09-105-537-5	Sequence 3, Appl	C 924	15	0.8	80	2	US-08-646-360-170	Sequence 170, App
C 852	16	0.8	38506	3	US-09-320-878-19	Sequence 3, Appl	C 925	15	0.8	80	3	US-08-839-765-119	Sequence 119, App
C 853	16	0.8	38506	4	US-09-141-908-1	Sequence 5, Appl	C 926	15	0.8	80	3	US-08-839-765-119	Sequence 119, App
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C 858	16	0.8	51259	3	US-08-781-891-209	Sequence 209, App	C 931	15	0.8	80	4	US-09-711-485-141	Sequence 141, App
C 859	16	0.8	51259	3	US-08-781-891-209	Sequence 209, App	C 932	15	0.8	80	4	US-09-711-485-141	Sequence 141, App
C 860	16	0.8	70000	4	US-09-851-896-3	Sequence 3, Appl	C 933	15	0.8	80	4	US-09-711-485-141	Sequence 141, App
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C 862	16	0.8	80595	3	US-09-078-294-4	Sequence 3, Appl	C 935	15	0.8	81	2	US-08-447-169A-143	Sequence 143, App
C 863	16	0.8	83450	4	US-09-811-459-3	Sequence 3, Appl	C 936	15	0.8	81	2	US-08-233-012C-143	Sequence 143, App
C 864	16	0.8	83450	4	US-10-370-659-3	Sequence 3, Appl	C 937	15	0.8	81	4	US-09-860-474-143	Sequence 143, App
C 865	16	0.8	87563	3	US-09-453-702B-57	Sequence 57, Appl	C 938	15	0.8	93	3	US-09-331-793-12	Sequence 3, App
C 866	16	0.8	95916	4	US-09-816-095-3	Sequence 3, Appl	C 939	15	0.8	94	4	US-08-976-413A-408	Sequence 408, App
C 867	16	0.8	107820	4	US-09-792-616-1	Sequence 1, Appl	C 940	15	0.8	94	4	US-09-513-999C-29269	Sequence 29269, App
C 868	16	0.8	116592	4	US-09-818-512-3	Sequence 3, Appl	C 941	15	0.8	99	4	US-09-270-767-79628	Sequence 29628, A
C 869	16	0.8	128779	4	US-09-497-855A-38	Sequence 38, Appl	C 942	15	0.8	101	4	US-09-877-243A-153	Sequence 153, App
C 870	16	0.8	148567	4	US-10-254-869-3	Sequence 3, Appl	C 943	15	0.8	101	4	US-09-513-999C-19621	Sequence 19621, App
C 871	16	0.8	148567	4	US-10-254-869-3	Sequence 3, Appl	C 944	15	0.8	117	3	US-09-513-999C-21164	Sequence 21164, A
C 872	16	0.8	193303	4	US-09-497-855A-37	Sequence 37, Appl	C 945	15	0.8	117	3	US-09-513-999C-36552	Sequence 36552, A
C 873	16	0.8	193303	4	US-09-497-855A-44	Sequence 44, Appl	C 946	15	0.8	127	3	US-08-857-046A-28	Sequence 28, Appl
C 874	16	0.8	202001	4	US-09-734-674-3	Sequence 3, Appl	C 947	15	0.8	157	4	US-09-621-976-7817	Sequence 7817, App
C 875	16	0.8	229354	4	US-09-765-400-64	Sequence 3, Appl	C 948	15	0.8	158	4	US-09-513-999C-11009	Sequence 11009, A
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C 877	16	0.8	320200	4	US-10-027-983-11	Sequence 11, Appl	C 950	15	0.8	176	4	US-09-270-767-2963	Sequence 2963, App
C 878	16	0.8	320200	4	US-09-198-452A-1	Sequence 1, Appl	C 951	15	0.8	180	4	US-09-331-793-19	Sequence 19, App
C 879	16	0.8	1664976	4	US-08-916-421B-1	Sequence 1, Appl	C 952	15	0.8	186	4	US-09-248-796A-7468	Sequence 7468, App
C 880	16	0.8	1664976	4	US-08-916-421B-1	Sequence 1, Appl	C 953	15	0.8	186	4	US-09-513-999C-18069	Sequence 18069, App
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C 883	15	0.8	18	3	US-09-289-466-52	Sequence 52, Appl	C 956	15	0.8	190	3	US-09-723-473-1	Sequence 473, App
C 884	15	0.8	18	4	US-09-478-189-28	Sequence 28, Appl	C 957	15	0.8	190	3	US-09-723-473-1	Sequence 473, App
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C 886	15	0.8	20	4	US-09-909-595-23	Sequence 23, Appl	C 959	15	0.8	192	4	US-09-248-796A-8239	Sequence 8239, App
C 887	15	0.8	26	2	US-08-497-997C-13	Sequence 13, Appl	C 960	15	0.8	192	4	US-09-248-796A-10135	Sequence 10135, App
C 888	15	0.8	27	3	US-09-036-579-11	Sequence 11, Appl	C 961	15	0.8	195	4	US-09-723-520-1	Sequence 1, Appl
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C 890	15	0.8	27	3	US-09-550-374-11	Sequence 11, Appl	C 963	15	0.8	199	4	US-09-513-999C-11157	Sequence 11157, A
C 891	15	0.8	27	3	US-09-943-906-11	Sequence 11, Appl	C 964	15	0.8	200	4	US-09-060-299-36	Sequence 36, Appl
C 892	15	0.8	35	3	US-09-397-885-13	Sequence 13, Appl	C 965	15	0.8	204	4	US-09-402-923A-36	Sequence 36, Appl
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C 894	15	0.8	35	3	US-09-397-885-13	Sequence 13, Appl	C 967	15	0.8	206	4	US-09-016-434-570	Sequence 570, App
C 895	15	0.8	36	1	US-09-969-362-13	Sequence 13, Appl	C 968	15	0.8	210	2	US-08-621-976-8995	Sequence 8995, App
C 896	15	0.8	36	1	US-07-960-510-12	Sequence 12, Appl	C 969	15	0.8	210	2	US-08-487-031-16	Sequence 16, Appl
C 897	15	0.8	36	1	US-07-960-510-12	Sequence 12, Appl	C 970	15	0.8	210	4	US-09-489-039A-6266	Sequence 6266, App
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980 15 0.8 213 4 US-09-513-999C-3200 Sequence 3200, Ap  
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984 15 0.8 219 3 US-09-466-138-19 Sequence 19, Appl  
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988 15 0.8 225 4 US-09-513-999C-13673 Sequence 13673, A  
989 15 0.8 226 4 US-09-513-999C-16872 Sequence 16872, A  
990 15 0.8 233 4 US-09-445-803-4 Sequence 4, Appl1  
991 15 0.8 234 4 US-09-489-039A-5121 Sequence 5121, Ap  
992 15 0.8 234 4 US-09-248-796A-7364 Sequence 7364, Ap  
993 15 0.8 235 4 US-09-621-976-13593 Sequence 13593, A  
994 15 0.8 241 4 US-09-389-681-334 Sequence 334, App  
995 15 0.8 241 4 US-09-620-405B-334 Sequence 334, App  
996 15 0.8 241 4 US-09-433-826B-334 Sequence 334, App  
997 15 0.8 241 4 US-09-604-287A-334 Sequence 334, App  
998 15 0.8 241 4 US-09-834-759-334 Sequence 334, App  
999 15 0.8 241 4 US-09-590-751A-334 Sequence 334, App  
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## ALIGNMENTS

RESULT 1  
US-08-306-691B-22  
Sequence 22, Application US/08306691B  
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APPLICANT: Skorski, Tomasz  
TITLE OF INVENTION: ANTISENSE  
TITLE OF INVENTION: OLIGONUCLEOTIDES TARGETING COOPERATING ONCOGENES  
NUMBER OF SEQUENCES: 55  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Seidel, Gonda, Lavorgna & Monaco, P.C.  
STREET: Two Penn Center, Suite 1800  
CITY: Philadelphia  
STATE: Pennsylvania  
COUNTRY: U.S.A.  
ZIP: 19102  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 720 KB  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
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TELEFAX: (215) 568-5549  
TELEX: No. 5734039e  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4626 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
US-08-306-691B-22

Query Match 1.2%; Score 23; DB 1; Length 4626;  
Best Local Similarity 100.0%; Pred. No. 0.33;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1240 AAGGTGCTGATTTGGCTTGC 1262  
|||||  
DB 3903 AAGGTGCTGATTTGGCTTGC 3925

## RESULT 2

PCT-US93-06251-27  
Sequence 27, Application PC/TUS9306251  
GENERAL INFORMATION:  
APPLICANT: Mickstrom, Eric and Rife, Jason P.  
TITLE OF INVENTION: Trivalent Synthesis of Oligonucleotides Containing  
Stereospecific Alkylphosphonates and Arylphosphonates  
NUMBER OF SEQUENCES: 93  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: SCULLY, SCOTT, MORPHY & PRESSER  
STREET: 400 Garden City Plaza  
CITY: Garden City  
STATE: NY  
COUNTRY: USA  
ZIP: 11530  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/06251  
FILING DATE: 19930630  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: DiGiulio, Frank S.  
REGISTRATION NUMBER: 31,346  
REFERENCE/DOCKET NUMBER: 8586  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 516-742-4343  
TELEFAX: 516-742-4366  
TELEX: 210 901 SANS UR  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4626 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
PCT-US93-06251-27  
Query Match 1.2%; Score 23; DB 5; Length 4626;  
Best Local Similarity 100.0%; Pred. No. 0.33;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1240 AAGGTGCTGATTTGGCTTGC 1262  
|||||  
DB 3903 AAGGTGCTGATTTGGCTTGC 3925

RESULT 3  
US-09-800-729-55  
Sequence 55, Application US/09800729  
Patent No. 6605592  
GENERAL INFORMATION:  
APPLICANT: Ni et al.  
TITLE OF INVENTION: 32 Human secreted proteins  
FILE REFERENCE: P2044P1  
CURRENT APPLICATION NUMBER: US/09/800,729  
CURRENT FILING DATE: 2001-03-08  
PRIOR APPLICATION NUMBER: PCT/US00/26013  
PRIOR FILING DATE: 2000-09-22  
PRIOR APPLICATION NUMBER: 60/155,709

PRIOR FILING DATE: 1999-09-24  
 NUMBER OF SEQ ID NOS: 217  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 55  
 LENGTH: 609  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: SITE  
 LOCATION: (554)  
 OTHER INFORMATION: n equals a,t,g, or c  
 US-09-800-729-55

Query Match 1.0%; Score 20; DB 4; Length 609;  
 Best Local Similarity 100.0%; Pred. No. 9.2;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 667 CACCTCTCCACCTCCACC 686  
 Db 269 CACCTCTCCACCTCCACC 288

RESULT 4  
 US-09-252-991A-1274  
 Sequence 1274, Application US/09252991A  
 Patent No. 6551795  
 GENERAL INFORMATION:  
 APPLICANT: Marc J. Rubenfield et al.  
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
 FILE REFERENCE: 107196.136  
 CURRENT APPLICATION NUMBER: US/09/252,991A  
 PRIOR FILING DATE: 1999-02-18  
 PRIOR APPLICATION NUMBER: US 60/074,788  
 PRIOR FILING DATE: 1998-02-18  
 PRIOR APPLICATION NUMBER: US 60/094,190  
 NUMBER OF SEQ ID NOS: 33142  
 SEQ ID NO 1274  
 LENGTH: 852  
 TYPE: DNA  
 ORGANISM: Pseudomonas aeruginosa  
 US-09-252-991A-1274

Query Match 1.0%; Score 20; DB 4; Length 852;  
 Best Local Similarity 100.0%; Pred. No. 9.2;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1467 GGCAGCAGCATTTGCTTAAC 1486  
 Db 56 GGCAGCAGCATTTGCTTAAC 75

RESULT 5  
 US-09-252-991A-1381/c  
 Sequence 1381, Application US/09252991A  
 Patent No. 6551795  
 GENERAL INFORMATION:  
 APPLICANT: Marc J. Rubenfield et al.  
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
 FILE REFERENCE: 107196.136  
 CURRENT APPLICATION NUMBER: US/09/252,991A  
 PRIOR FILING DATE: 1999-02-18  
 PRIOR APPLICATION NUMBER: US 60/074,788  
 PRIOR FILING DATE: 1998-02-18  
 PRIOR APPLICATION NUMBER: US 60/094,190  
 NUMBER OF SEQ ID NOS: 33142  
 SEQ ID NO 1381  
 LENGTH: 909  
 TYPE: DNA  
 ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-1381

Query Match 1.0%; Score 20; DB 4; Length 909;  
 Best Local Similarity 100.0%; Pred. No. 9.2;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1467 GGCAGCAGCATTTGCTTAAC 1486  
 Db 112 GGCAGCAGCATTTGCTTAAC 93

RESULT 6  
 US-09-252-991A-1287/c  
 Sequence 1287, Application US/09252991A  
 Patent No. 6551795  
 GENERAL INFORMATION:  
 APPLICANT: Marc J. Rubenfield et al.  
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
 FILE REFERENCE: 107196.136  
 CURRENT APPLICATION NUMBER: US/09/252,991A  
 PRIOR FILING DATE: 1999-02-18  
 PRIOR APPLICATION NUMBER: US 60/074,788  
 PRIOR FILING DATE: 1998-02-18  
 PRIOR APPLICATION NUMBER: US 60/094,190  
 NUMBER OF SEQ ID NOS: 33142  
 SEQ ID NO 1287  
 LENGTH: 1092  
 TYPE: DNA  
 ORGANISM: Pseudomonas aeruginosa  
 US-09-252-991A-1287

Query Match 1.0%; Score 20; DB 4; Length 1092;  
 Best Local Similarity 100.0%; Pred. No. 9.2;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1467 GGCAGCAGCATTTGCTTAAC 1486  
 Db 126 GGCAGCAGCATTTGCTTAAC 107

RESULT 7  
 US-09-248-796A-4378  
 Sequence 4378, Application US/09248796A  
 Patent No. 6747137  
 GENERAL INFORMATION:  
 APPLICANT: Keith Weinstock et al  
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS  
 FILE REFERENCE: 107196.132  
 CURRENT APPLICATION NUMBER: US/09/248,796A  
 PRIOR FILING DATE: 1999-02-12  
 PRIOR APPLICATION NUMBER: US 60/074,725  
 PRIOR FILING DATE: 1998-02-13  
 PRIOR APPLICATION NUMBER: US 60/096,409  
 PRIOR FILING DATE: 1998-08-13  
 NUMBER OF SEQ ID NOS: 28208  
 SEQ ID NO 4378  
 LENGTH: 1680  
 TYPE: DNA  
 ORGANISM: Candida albicans  
 US-09-248-796A-4378

Query Match 1.0%; Score 20; DB 4; Length 1680;  
 Best Local Similarity 100.0%; Pred. No. 9.2;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1244 TTGCTATTTGGTCTTGCT 1263  
 Db 866 TTGCTATTTGGTCTTGCT 885

RESULT 8  
US-09-248-796A-1640  
; Sequence 1640, Application US/09248796A  
; Patent No. 6747137  
; GENERAL INFORMATION:  
; APPLICANT: Keith Weinstock et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS  
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.132  
; CURRENT APPLICATION NUMBER: US/09/248,796A  
; CURRENT FILING DATE: 1999-02-12  
; PRIOR APPLICATION NUMBER: US 60/074,725  
; PRIOR FILING DATE: 1998-02-13  
; PRIOR APPLICATION NUMBER: US 60/096,409  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 28208  
; SEQ ID NO 1640  
; LENGTH: 2838  
; TYPE: DNA  
; ORGANISM: Candida albicans  
US-09-248-796A-1640

Query Match  
Best Local Similarity 1.0%; Score 20; DB 4; Length 2838;  
Best Local Similarity 100.0%; Pred. No. 9.2;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 670 CCTCTCCACCTCCACCACC 689  
DB 1114 CCTCTCCACCTCCACCACC 1133

RESULT 9  
US-09-228-986-11  
; Sequence 11, Application US/09228986  
; Patent No. 6359198  
; GENERAL INFORMATION:  
; APPLICANT: Strabala, Timothy  
; APPLICANT: Nieuwenhuizen, Niels  
; TITLE OF INVENTION: Compositions Isolated from Plant Cells  
; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling  
; FILE REFERENCE: 11000/1020  
; CURRENT APPLICATION NUMBER: US/09/228,986  
; CURRENT FILING DATE: 1999-01-12  
; NUMBER OF SEQ ID NOS: 130  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 11  
; LENGTH: 3097  
; TYPE: DNA  
; ORGANISM: Eucalyptus grandis  
US-09-228-986-11

Query Match  
Best Local Similarity 1.0%; Score 20; DB 3; Length 3097;  
Best Local Similarity 100.0%; Pred. No. 9.2;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1387 GTTGCTTTGGAGCTCAT 1406  
DB 2556 GTTGCTTTGGAGCTCAT 2575

RESULT 10  
US-10-101-464A-11  
; Sequence 11, Application US/10101464A  
; Patent No. 6768041  
; GENERAL INFORMATION:  
; APPLICANT: Strabala, Timothy  
; APPLICANT: Nieuwenhuizen, Nicolaas  
; APPLICANT: Higgins, Colleen M.  
; TITLE OF INVENTION: Compositions Isolated from Plant Cells  
; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling  
; FILE REFERENCE: 11000.1020c2  
; CURRENT APPLICATION NUMBER: US/10/101,464A  
; CURRENT FILING DATE: 2002-03-18

; PRIOR APPLICATION NUMBER: 09/704,302  
; PRIOR FILING DATE: 2000-11-01  
; PRIOR APPLICATION NUMBER: 09/228,986  
; PRIOR FILING DATE: 1999-01-12  
; PRIOR APPLICATION NUMBER: 60/162,866  
; PRIOR FILING DATE: 1999-11-01  
; PRIOR APPLICATION NUMBER: PCT/US00/00724  
; PRIOR FILING DATE: 2000-01-11  
; NUMBER OF SEQ ID NOS: 989  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 11  
; LENGTH: 3097  
; TYPE: DNA  
; ORGANISM: Eucalyptus grandis  
US-10-101-464A-11

Query Match  
Best Local Similarity 1.0%; Score 20; DB 4; Length 3097;  
Best Local Similarity 100.0%; Pred. No. 9.2;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1387 GTTGCTTTGGAGCTCAT 1406  
DB 2556 GTTGCTTTGGAGCTCAT 2575

RESULT 11  
US-09-800-729-18  
; Sequence 18, Application US/09800729  
; Patent No. 6605592  
; GENERAL INFORMATION:  
; APPLICANT: Ni et al.  
; TITLE OF INVENTION: 32 Human secreted proteins  
; FILE REFERENCE: P2044p1  
; CURRENT APPLICATION NUMBER: US/09/800,729  
; CURRENT FILING DATE: 2001-03-08  
; PRIOR APPLICATION NUMBER: PCT/US00/26013  
; PRIOR FILING DATE: 2000-09-22  
; PRIOR APPLICATION NUMBER: 60/155,709  
; PRIOR FILING DATE: 1999-09-24  
; NUMBER OF SEQ ID NOS: 217  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 18  
; LENGTH: 5720  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-800-729-18

Query Match  
Best Local Similarity 1.0%; Score 20; DB 4; Length 5720;  
Best Local Similarity 100.0%; Pred. No. 9.2;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 667 CAACCTCCACCTCCACC 686  
DB 5431 CAACCTCCACCTCCACC 5450

RESULT 12  
US-09-755-665-46/c  
; Sequence 46, Application US/09755665  
; Patent No. 6600019  
; GENERAL INFORMATION:  
; APPLICANT: Prayaga, Sudhirdas K.  
; APPLICANT: Majumder, Kumud  
; APPLICANT: Tallion, Bruce E.  
; APPLICANT: Spaderna, Steven K.  
; APPLICANT: Spytek, Kimberly A.  
; APPLICANT: MacDougall, John  
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME  
; FILE REFERENCE: 15966-631  
; CURRENT APPLICATION NUMBER: US/09/755,665  
; CURRENT FILING DATE: 2001-08-14  
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/174,724  
; PRIOR FILING DATE: 2000-01-06

NUMBER OF SEQ ID NOS: 118  
SOFTWARE: Patent In Ver. 2.1  
SEQ ID NO: 46  
LENGTH: 41100  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: GENOMIC DNA  
US-09-755-665-46

Query Match 1.0%; Score 19; DB 4; Length 41100;  
Best Local Similarity 100.0%; Pred. No. 9.2;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 921 TGGGAGTGTCTCGGAGAGA 940  
DB 22048 TGGGAGTGTCTCGGAGAGA 22029

RESULT 13

US-08-991-789A-168  
Sequence 168, Application US/08991789A  
Patent No. 6225054  
GENERAL INFORMATION:  
APPLICANT: Fridakis, Tony N.  
Smith, John M.  
Reed, Steven G.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
TREATMENT AND DIAGNOSIS OF BREAST CANCER  
NUMBER OF SEQUENCES: 292  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Seed IP Law Group  
STREET: 701 Fifth Avenue, Suite 6300  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98104-7092

COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/991,789A  
FILING DATE: 11-Dec-1997

CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Potter, Jane E. R.  
REGISTRATION NUMBER: 33,332  
REFERENCE/DOCKET NUMBER: 210121.419C3  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 168:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 358 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 168:  
US-08-991-789A-168

Query Match 1.0%; Score 19; DB 3; Length 358;  
Best Local Similarity 100.0%; Pred. No. 28;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 950 AGGCAGAGTTGAGATCAT 968  
DB 228 AGGCAGAGTTGAGATCAT 246

RESULT 14  
US-09-062-451-168

Sequence 168, Application US/09062451  
Patent No. 6344550  
GENERAL INFORMATION:  
APPLICANT: Fridakis, Tony N.  
Smith, John M.  
Reed, Steven G.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
TREATMENT AND DIAGNOSIS OF BREAST CANCER  
NUMBER OF SEQUENCES: 297  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: SEED AND BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98104-7092

COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/062,451  
FILING DATE: 04-APR-1997

CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Makl, David J.  
REGISTRATION NUMBER: 31,392  
REFERENCE/DOCKET NUMBER: 210121.419C2  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 168:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 358 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

US-09-062-451-168

Query Match 1.0%; Score 19; DB 3; Length 358;  
Best Local Similarity 100.0%; Pred. No. 28;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 950 AGGCAGAGTTGAGATCAT 968  
DB 228 AGGCAGAGTTGAGATCAT 246

RESULT 15  
US-09-598-326-168  
Sequence 168, Application US/09598326  
Patent No. 6423496  
GENERAL INFORMATION:  
APPLICANT: Fridakis, Tony N.  
Smith, John M.  
Reed, Steven G.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
TREATMENT AND DIAGNOSIS OF BREAST CANCER  
NUMBER OF SEQUENCES: 247  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Seed Intellectual Property Law Group PLLC  
STREET: 701 Fifth Avenue, Suite 6300  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98104-7092

COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/598,326  
 FILING DATE: 20-Jun-2000  
 CLASSIFICATION: <Unknown>  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Potter, Jane E.R.  
 REGISTRATION NUMBER: 33,332  
 REFERENCE/DOCKET NUMBER: 210121.419D1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (206) 622-4900  
 TELEFAX: (206) 682-6031  
 INFORMATION FOR SEQ ID NO: 168:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 358 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 SEQUENCE DESCRIPTION: SEQ ID NO: 168:  
 US-09-598-326-168

Query Match 1.0%; Score 19; DB 4; Length 358;  
 Best Local Similarity 100.0%; Pred.No.28;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 950 AGGAGAGGTTGAGATCAT 968  
 |||||  
 Db 228 AGGAGAGGTTGAGATCAT 246

Search completed: November 13, 2004, 15:32:42  
 Job time : 150 secs



Query Match 100.0%; Score 1944; DB 6; Length 1944;

Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1944; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGCTCGGCGCGCTCTCGGGGACTGTTGCGCTCCATCTCCACCATCAAACTGACAA 60
Db 1 ATGCTCGGCGCGCTCTCGGGGACTGTTGCGCTCCATCTCCACCATCAAACTGACAA 60
QY 61 ACCACGACTCTCTCTCGAGCTTCGCTCCCTCTCCACCAACACTTCTCTCTCGGCG 120
Db 61 ACCACGACTCTCTCTCGAGCTTCGCTCCCTCTCTCCACCAACACTTCTCTCTCGGCG 120
QY 121 CCATCCACTATTCCGACATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 180
Db 121 CCATCCACTATTCCGACATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 180
QY 181 CCATCTCCACCACTCATCTTAAGCGGGGATCTCCACCTCTCTCTCTCTCTCTCTCA 240
Db 181 CCATCTCCACCACTCATCTTAAGCGGGGATCTCCACCTCTCTCTCTCTCTCTCTCA 240
QY 241 CCGGCTCCAACTACGCGCGGATCTCCACCGGCACTGTACTCTCTCTCTCTCTCTCT 300
Db 241 CCGGCTCCAACTACGCGCGGATCTCCACCGGCACTGTACTCTCTCTCTCTCTCTCT 300
QY 301 CCACCTTCAGTCCAGGACCAACCGTCCATCTCTCAAGCGAAGAGATCTCTCGACT 360
Db 301 CCACCTTCAGTCCAGGACCAACCGTCCATCTCTCAAGCGAAGAGATCTCTCGACT 360
QY 361 CCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 420
Db 361 CCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 420
QY 421 GGAATCGCCATCGGAGAGTCTGCTGTGTGATGATGATGATGATGATGATGATGAT 480
Db 421 GGAATCGCCATCGGAGAGTCTGCTGTGTGATGATGATGATGATGATGATGATGAT 480
QY 481 AAGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
Db 481 AAGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
QY 541 GGTGCCAAAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
Db 541 GGTGCCAAAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
QY 601 ACACCAACCTCAGATCATCTGCTGATGATGATGATGATGATGATGATGATGATGAT 660
Db 601 ACACCAACCTCAGATCATCTGCTGATGATGATGATGATGATGATGATGATGATGAT 660
QY 661 CCAAGGCAACCTCTCTCACTCTCACTCACTCACTCACTCACTCACTCACTCACTCACT 720
Db 661 CCAAGGCAACCTCTCTCACTCTCACTCACTCACTCACTCACTCACTCACTCACTCACT 720
QY 721 TACTCGGACCGTCCAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 780
Db 721 TACTCGGACCGTCCAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 780
QY 781 AGCACTTTCACATACGAGAGAGTACTAGAGCCCAATGGTCTCTCGAGGCAACTTG 840
Db 781 AGCACTTTCACATACGAGAGAGTACTAGAGCCCAATGGTCTCTCGAGGCAACTTG 840
QY 841 TTAGGACAGGCGGCGGTTGCTTACGTGCAAAAGGTGTGCTCTAGTGGGAAAGATT 900
Db 841 TTAGGACAGGCGGCGGTTGCTTACGTGCAAAAGGTGTGCTCTAGTGGGAAAGATT 900
QY 901 GCTGTGAAGAGTGAAGATTGGAGTGTGTCAGGAGAGAGAGAGAGAGATTGAGGAGATT 960
Db 901 GCTGTGAAGAGTGAAGATTGGAGTGTGTCAGGAGAGAGAGAGAGATTGAGGAGATT 960
QY 961 GAGATCATACGACAGAGTTCACCAAGGATCTGGGTCTCTGTTGTTATGATGATGCC 1020
Db 961 GAGATCATACGACAGAGTTCACCAAGGATCTGGGTCTCTGTTGTTATGATGATGCC 1020
QY 1021 GGTGCCAAAGAGATTGCTTGTATGATGATTGTTCTTAAACAATCTGAGCTTCACTTC 1080
Db 1021 GGTGCCAAAGAGATTGCTTGTATGATGATTGTTCTTAAACAATCTGAGCTTCACTTC 1080
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Db 1021 GGTGCCAAAGAGATTGCTTGTATGATGATTGTTCTTAAACAATCTGAGCTTCACTTC 1080
QY 1081 CATGGCGAGGAGCGGCTTCAATGGAATGAGACACAGATTGAGATTGCTTGTGATCT 1140
Db 1081 CATGGCGAGGAGCGGCTTCAATGGAATGAGACACAGATTGAGATTGCTTGTGATCT 1140
QY 1141 GCTAAAGACTTTCATCTTCAATGGAATGGAATCTTAAATCACTTCAACGATATTC 1200
Db 1141 GCTAAAGACTTTCATCTTCAATGGAATGGAATCTTAAATCACTTCAACGATATTC 1200
QY 1201 AAGGCTTCAAAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1260
Db 1201 AAGGCTTCAAAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1260
QY 1261 GCTAAGATTGCTTCTGATCAAAACAGCATGATCAACAGTGTGATGAGGAACTTTGG 1320
Db 1261 GCTAAGATTGCTTCTGATCAAAACAGCATGATCAACAGTGTGATGAGGAACTTTGG 1320
QY 1321 TACTTGCTCCGGAATACGCTGCAAGCGGAAAGCTCAAGGAAAGTCTGATCTTTCTCA 1380
Db 1321 TACTTGCTCCGGAATACGCTGCAAGCGGAAAGCTCAAGGAAAGTCTGATCTTTCTCA 1380
QY 1381 TTGCGGTTGTGCTTTTGGAGCTCATTTACTGAGCGTGACCCGTTGATGCAACAATGTC 1440
Db 1381 TTGCGGTTGTGCTTTTGGAGCTCATTTACTGAGCGTGACCCGTTGATGCAACAATGTC 1440
QY 1441 TATGTAGATGACAGTCTTATGATGATGATGATGATGATGATGATGATGATGATGAT 1500
Db 1441 TATGTAGATGACAGTCTTATGATGATGATGATGATGATGATGATGATGATGATGAT 1500
QY 1501 GGAAGCTTTGAGGCTTTAGCTGATGCAAAAGATGAATTAATGATGATGATGATGATG 1560
Db 1501 GGAAGCTTTGAGGCTTTAGCTGATGCAAAAGATGAATTAATGATGATGATGATGATG 1560
QY 1561 GCTGCAATGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1620
Db 1561 GCTGCAATGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1620
QY 1621 ATGAGCCAGATTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680
Db 1621 ATGAGCCAGATTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680
QY 1681 ATGAGACCAAGTCAAAAGCATATGATACAGCTCATGAGGAGGAGGAGGAGGAGGAG 1740
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QY 1741 AGCCAGTACATGAGAGCATGAGAAAGTTTGAAGAAATGCACTTGAACCTCAAGATAC 1800
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QY 1801 AACGCCACGGGTGATGATCAAGTATCCGACCAAGTACTATGATGATCCGCTTGTGTTCA 1860
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QY 1861 AGCAGCGAGGCGCCAAACCAACGCGGAATGAGATGAGGAAATTTAAGAGAACGGGTGAG 1920
Db 1861 AGCAGCGAGGCGCCAAACCAACGCGGAATGAGATGAGGAAATTTAAGAGAACGGGTGAG 1920
QY 1921 GGTATATGTGACCTTCTCTTTAA 1944
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RESULT 2  
AX825703 1944 bp DNA linear PAT 11-DEC-2003  
LOCUS  
DEFINITION Sequence 1 from Parent W003072763.  
ACCESSION AX825703  
VERSION AX825703.1 GI:39751230  
KEYWORDS  
SOURCE  
ORGANISM  
Brassica napus (rape)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;



QY 1681 ATGAGACCAAGTCAAGCAATGTATACAGCTTACACGAGGAGGAGCAAGCAATTATGACTCG 1740  
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DB 1801 AACGCCAGCGGTGAGTACAGTATCCGACGAGTACTATGACTGTATCCCGTCTGGTTCA 1860  
QY 1861 AGCAGGAGGAGGAGCAACCAACGAGCAATGAGATGGGAGATTAAAGAAACCGGTACG 1920  
DB 1861 AGCAGGAGGAGGAGCAACCAACGAGCAATGAGATGGGAGATTAAAGAAACCGGTACG 1920  
QY 1921 GGTATAGTGAACCTTCTCTTTAA 1944  
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RESULT 3  
AX825705 2189 bp DNA linear PAT 11-DEC-2003  
DEFINITION Sequence 3 from Patent W003072763.  
ACCESSION AX825705  
VERSION AX825705.1 GI:39751232  
KEYWORDS  
SOURCE Brassica napus (rape)  
ORGANISM Brassica napus  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosids; eustosids II; Brassicales; Brassicaceae; Brassica.  
1  
REFERENCE  
AUTHORS Goring, D., Silva, N. and Haffani, Y. Z.  
TITLE Increasing plant seed production  
PATENT: WO 03072763-A 3 04-SEP-2003;  
JOURNAL Goring, Daphne (CA) ; Silva, Nancy (CA) ; Haffani, Yosr, Z. (CA)  
LOCATION/Qualifiers  
FEATURES  
source 1. .2189  
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/mol\_type="unassigned DNA"  
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ORIGIN  
Query Match 100.0%; Score 1944; DB 6; Length 2189;  
Best local Similarity 100.0%; Pred. No. 0;  
Matches 1944; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTCTCGGCGCGCTCTCCGGGAGCTGCTGCTCATCTCCACCATCAAACTCCACA 60  
DB 97 ATGTCTCGGCGCGCTCTCCGGGAGCTGCTGCTCATCTCCACCATCAAACTCCACA 156  
QY 61 ACCAGCACTCTCTCCAGCTTCCGCTCTCTCTCCACACACACCTTCTCTCCGCG 120  
DB 157 ACCAGCACTCTCTCTCCAGCTTCCGCTCTCTCTCCACACACACCTTCTCTCCGCG 216  
QY 121 CCATCCATATTCGACATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 180  
DB 217 CCATCCATATTCGACATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 276  
QY 181 CCATCTCAACCACTTCAATTCACGCGGGATCTCCACCTCTCTCTCTCTCTCTCTCT 240  
DB 277 CCATCTCAACCACTTCAATTCACGCGGGATCTCCACCTCTCTCTCTCTCTCTCTCT 336  
QY 241 CCGGCTCAACCTTCAACCTTCAACCTTCAACCTTCAACCTTCAACCTTCAACCTT 300  
DB 337 CCGGCTCAACCTTCAACCTTCAACCTTCAACCTTCAACCTTCAACCTTCAACCTT 396  
QY 301 CCACCTTCAAGTCCAGGACCAACCTTCAACCTTCAACCTTCAACCTTCAACCTT 360  
DB 397 CCACCTTCAAGTCCAGGACCAACCTTCAACCTTCAACCTTCAACCTTCAACCTT 456

QY 361 CCATCTTCTCCCTCCGCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 420  
DB 457 CCATCTTCTCCCTCCGCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 516  
QY 421 GGAATCGCATTCGAGAGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 480  
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DB 577 AAGAAGAAACGAGAGAGACGAGAGATGCTTCTATGTTCTCTCCGACCTCTCTCT 636  
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QY 901 GCTGTGAGAGATTTGAAAGTTGGAGATGCTCAGGAGAGAGGAGTTTCAAGAGAGTT 960  
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DB 1357 GCTAAGATTTCTTATGATTTTCTTAAACAAGGATGATTTCAACGTTGATGAGAACTTGG 1416  
QY 1321 TACTTGGCTCGGAAATATGCTGCAAGCGAAAGCTCAAGGAGAGTCTGAGTTTCTCA 1380  
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QY 1381 TTGCGCTTGTCTTGTGAGTCTTAACTGAGCTGACCGCTTGTGATGCTCAACAATGTC 1440  
DB 1477 TTGCGCTTGTCTTGTGAGTCTTAACTGAGCTGACCGCTTGTGATGCTCAACAATGTC 1536



QY 901 GCTGTGAACAGATTGAAGTTGGAGTGGTCAAGGAGAGAGGAGTTTCAGGAGAGGTT 960  
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QY 1021 GGTGCCAAAAGATTGGTGTCTATGAGTTGTTCTTAAACAACATCTCGAGCTTCACTTC 1080  
Db 1117 GGTGCCAAAAGATTGGTGTCTATGAGTTGTTCTTAAACAACATCTCGAGCTTCACTTC 1176  
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QY 1201 AAGGCTTCAACATTTGATGATTTCAAGTTGAAGTTGAAGTTGCTGATTTGGTCTT 1260  
Db 1297 AAGGCTTCAACATTTGATGATTTCAAGTTGAAGTTGAAGTTGCTGATTTGGTCTT 1356  
QY 1261 GCTAAAGAGCTTCTGATCAACAGAGATTTCAACAGATTTGAAGTTGAAGTTGGAGCTTGGG 1320  
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Db 1417 TACTTGGCTCCGGAATACGCTGCAAGGAGGAGGAGTCAAGGAGAGTCTGAGCTTTCTCA 1476  
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Db 1477 TTTGGGCTTGTGCTTTTGAAGTCTATTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1536  
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Db 1537 TATGTAGATGACAGCTTGTGATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1596  
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QY 1681 ATGAGCCAGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1740  
Db 1777 ATGAGCCAGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1836  
QY 1741 AGCCAGATGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 1800  
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Db 1897 AAGCCAGAGGAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1956  
QY 1861 AGCAGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1920  
Db 1957 AGCAGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2016  
QY 1921 GGTATATGATGAGCTTCTCTTTAA 1944  
Db 2017 GGTATATGATGAGCTTCTCTTTAA 2040

RESULT 5  
AX825738 1959 bp DNA linear PAT 11-DEC-2003  
LOCUS AX825738  
DEFINITION Sequence 36 from Patent WO03072763.  
ACCESSION AX825738  
VERSION AX825738.1 GI:39751255  
KEYWORDS  
SOURCE  
ORGANISM  
Arabidopsis thaliana (thale cress)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
REFERENCE  
1 Goring, D., Silva, N. and Haffani, Y. Z.  
Increasing plant seed production.  
Patent: WO 03072763-A 36 04-SEP-2003;  
Goring, Daphne (CA); Silva, Nancy (CA); Haffani, Yost, Z. (CA)  
Location/Qualifiers  
1..1959  
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FEATURES  
source  
ORIGIN  
Query Match 70.4%; Score 1369.4; DB 6; Length 1959;  
Best Local Similarity 83.4%; Pred. No. 3.1e-269;  
Matches 1611; Conservative 0; Mismatches 291; Indels 30; Gaps 4;  
QY 31 TCGCTTCATCTCCACCATTAACCTCCACACACACCTCCCTCCAGCTTCGCGCTCT 90  
Db 40 TCTCCACCGCTCTCTCCACCAACTGACACACACACCTCTCTCCACAGAGCTCTCT 99  
QY 91 CCTCCACACACAC-----CTCTCTCTCTCCGCGCATCACTATTTCCGACATCT 141  
Db 100 CTTCTCTCCACACACACT 159  
QY 142 CTTCT 201  
Db 160 CTTCT 219  
QY 202 ACGCGGAGATCTCCACT 261  
Db 220 A-----CT 267  
QY 262 TCTCCACCGCAGCT 321  
Db 268 CCACT 327  
QY 322 CCGTCCATCT 381  
Db 328 CCAACACT 387  
QY 382 TCT 441  
Db 388 TCTGATCT 447  
QY 442 GCTCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 498  
Db 448 GCTATCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 507  
QY 499 ---GAGGAGAGATGCTTACTATGTTCTCTGCACTCTCTCTCTCTCTCTCTCTCTCTCT 555  
Db 508 CAGACAGATGAAGCTGCTTACTATGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 567  
QY 556 GGAACCTTAAGCTGAGACAGACACCAATGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 615  
Db 568 GGAACCTTAAGCTGAGACACCAATGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 627  
QY 616 CATGTCGAT 675  
Db 628 AATCATGAT 687











## ORIGIN

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Query Match 70.4%; Score 1369.4; DB 8; Length 2188;  
 Best Local Similarity 83.4%; Pred. No. 3,1e-269;  
 Matches 1611; Conservative 0; Mismatches 291; Indels 30; Gaps 4;

QY 31 TCGCCCTCACTCCACATCAAACTCCACAAACACAGACTCCCTCCAGCTCCGCTCT 90  
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 Db 131 CCTCTCCACGACACATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 190  
 QY 142 CCT 201  
 Db 191 CCT 250  
 QY 202 AGCGCGGATCTCAACCT 261  
 Db 251 A-----CT 298  
 QY 262 TCTCCACCGGACCTGTTAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 321  
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 QY 332 CGGTCCAACTCTTCAAGGAGAGATCTCTCGACTCTCTCTCTCTCTCTCTCTCTCT 381  
 Db 339 CCAAACT 418  
 QY 382 TCT 441  
 Db 419 TCTGATTTCTCGATGATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 478  
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 Db 479 GCTATTTCTGTTAATCTGATTTGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 538  
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 QY 1213 AATTTGATGATTTCAAGTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1272  
 Db 1259 AATTTGATGATTTCAAGTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1318  
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 Db 1859 GAGTACAGTATTCGACCAAGTGAATGATGATGATGATGATGATGATGATGATGATGATG 1918  
 QY 1873 CAAACCAACGCGAATGAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1932  
 Db 1919 CAAACCAACGCGAATGAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1978  
 QY 1933 CTTTCTCTTTAA 1944  
 Db 1979 CCTCTCTTTAA 1990

RESULT 9  
 AY093065







## ORIGIN

Query Match 70.4%; Score 1367.8; DB 8; Length 1959;  
Best Local Similarity 83.3%; Pied. No. 6.6e-269;  
Matches 1610; Conservative 0; Mismatches 292; Indels 30; Gaps 4;

31 TGGCTTCATCTCCACATCAAACTCCACAACCAACCACTCTCTCCAGCTTCGGCTCT 90  
40 TCTCCACCGCTCTCTCCCAAACTCGACACCAACCACTCTCTCTCCAGAGCTCTCT 99  
91 CCTCCACCAACAC-----CTTCTCTCTCCCGCCGCACTCATCTATTCGACATCT 141  
100 CTTCTCTCCCAACAACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 159  
142 CTTCT 201  
160 CTTCT 219  
202 AGCCGGGATCTCCACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 261  
220 A-----CT 267  
262 TCTCCACCGCACT 321  
268 CCAACCGCTCTCCACCAACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 327  
322 CCGTCCATCT 381  
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628 AATCATGATGAGCTGATCTGCTACCTCAACCTCTCTCTCTCTCTCTCTCTCTCT 687  
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748 CCGGTTCT 807  
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868 GGGTGTGTTATGCTATGAAGATATATGCTCTCTCTCTCTCTCTCTCTCTCTCT 927  
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988 AGAGTTCAACCAAGGCTATGCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1047

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1348 GAATACGCTGCAAGCGGAAAGCTCAGGAGAGAGCTGACGCTTTTCTCATTTTGGCGTTGTG 1407  
1393 CTTTGGAGCTCATTTCTGAGCGTCAACCGCTTGAATGCCAACAATGCTCTATGATGATGAC 1452  
1408 CTTTGGAGCTCATTTCTGAGCGCGCTGTTGATGATGCCAACAATGCTCTATGATGATGAC 1467  
1453 AGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1512  
1468 AGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1527  
1513 GGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1572  
1528 GGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1587  
1573 GGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1632  
1588 GGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1647  
1633 GTGGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1692  
1648 GTAGGCGGTTAGAGAGAAATGATGCTGCTGATGATGATGATGATGATGATGATGATGAT 1707  
1693 CAAAGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1752  
1708 CACAGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1767  
1753 GAAGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1812  
1768 GACGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1827  
1813 GAGTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1872  
1828 GAGTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1887  
1873 CAAACCAACGCGAATGAGATGAGAGGAGATTAAAGAACCGGCTCAGGGTTATGATGGA 1932  
1888 CAAAGCAACGCGAATGAGATGAGAGGAGATTAAAGAACCGGCTCAGGGTTATGATGGA 1947  
1933 CTTTCTCTTTAA 1944  
1948 CCTCTCTTTAA 1959

RESULT 11  
BT008409 1959 bp mRNA linear PUN 15-MAY-2003  
LOCUS Arabidopsis thaliana At3g24600 gene, complete cds.  
DEFINITION Arabidopsis thaliana At3g24600 gene, complete cds.  
ACCESSION BT008409  
VERSION BT008409.1 GI:30725491  
KEYWORDS FLI\_CDNA.







QY	91	CCGCCACACACAC-----CTCTCTCTCCCGCGCGGACATCCATCTATCCGACATCT	141
Db	206	CTCTCTCCACACACAACTCTTTTCTCTCTCCGCGCGGACATCCATCTATCCACCTCT	265
QY	142	CCTCTCTCTTCTCTCTCTCTACACCTTCTGCTCTCTCTCTCATCTCTCACCAATCTCATCT	201
Db	266	CTCTCTCTCTCTCTCTCTTACTCTCTGTCTTCTCTCTCATCTCTCTCTGATCTTTA	325
QY	202	AGCGCGGATCTTCACCTCTCTCTCTCAGCGTCTTCACCGCGCTCAACTACGCGCGA	261
Db	326	A-----CTCTCTCTATCTCTCAACCTTCCCGCTCTCCATCTCATCTCTCT	373
QY	262	TCGCCACCGCACCTGTACTCTCTCTACCTCGAAACCTTCACCTTCAGTCCGAGACCA	321
Db	374	CCACGCTCCACACACACACCTCTCAACCTTCGAGCGCTCTCATCTCTCAACAGACCA	433
QY	322	CCGTCOAATCTTTCACGCGAAGAGATCTCTCGACCTTCATCTTCTCTCTCGCGCG	381
Db	434	CCAAACACTCTCTCAGGATCTACTCTTAAGTCTCATCAACCTMAACCTMAACGTCGCGCG	493
QY	382	TCTCCCTTTCGACGCGTTATTCACAGAGATGTGTGGAAATGCCATTCGAGAGATC	441
Db	494	TCGTATCTTCCGAGAGATGTCTACCGGAGTTGTGTAGGATCCCATTTGAGAGATC	553
QY	442	GCTCTGTGTATGTAGTCACTCTGTATTTGTCTCTCTGTAAAGAAAGACGAGAA---	498
Db	554	GCTATCTTGTATTACTGACTCTGTATTTGTCTCTCTGTAAAGAAAGAAAGAAAGA	613
QY	499	---GACGAAAGATGCTTACTATGTCTCTCGGCACTCTCTCTCTGTGTCCAAAGCGGA	555
Db	614	CACGAGATGAAGGCTTACTATGTCTCTCTCTCTCTCACTGTGTCCAAAGCTGTGA	673
QY	556	GGACCTTACGCTGACAGAGACAATGGCGGCAACAAAGGCAACACACCGTACAT	615
Db	674	GGACTTACGCTGACAGAGACAATGGCGGCAACAAAGGCAACACACCGTACAT	733
QY	616	CATGTCGTGACGTCACTACCAACCACTTAAGGCTTCATCTCCACACGAGAACCTCT	675
Db	734	AATCATGTAGTACGTCACTACCAACCACTTAAGGCTTCATCTCCACACGAGAACCTCT	793
QY	676	---CCACCTCACACCGGCTTTCATGAGGACACAGCGGCGTCCGACTACTCCGACCT	732
Db	794	CCGCACTTCACACACACGATTCATGATACAGGCGGTCTGTGACTATTCGATCTT	853
QY	733	CCAGTCTCTCTCCACGCTCTCCAGGCTTGTGTAGGCTTCTCCAAAGCACTTTCACA	792
Db	854	CCGCTTCTCTCTCCACGCTCTCCAGGCTTGTGTAGGCTTCTCCAAAGCACTTTCACT	913
QY	793	TACAGAGAGCTAGCTAGAGCCCAATGTTTCTCGAAGCGAATTGTTAGACACAGC	852
Db	914	TATAGAGAGGTTGTCAAGAGCTATCTAATGCTTCTCTGAGGCTAATTTGTTAGACACAGG	973
QY	853	GCGTTGCGTTACGTCAACAAAGGTGTGTGCTTAGGGGAAAGAAAGTGTGTGAACAG	912
Db	974	GCGTTGCGTTATGTCTCAATTAAGGTATATGCTTAGGGGAAAGAAAGTGTGTGAACAG	1033
QY	913	TTGAAGTTGGAGTGTCTAGGAGAGAGAGGATTTCAAGCAGAGATTGAATCATCAGC	972
Db	1034	TTGAAGTTGGAGTGTCTAGGAGAGAGAGGATTTCAAGCAGAGATTGAATCATCAGC	1099
QY	973	AGAGTTCAACAAGGCACTGTGTCTTGTGTATTTGTGATGTGCGGTGTCCAAAGA	1033
Db	1094	AGAGTTCAACAAGGCACTTTGTGTCTTATTTGTATTTGTATGTGCGGTGTCCAAAGA	1155
QY	1033	TTGCTGTCTATGATTTGTCTTAACAACATCTCGAGTTCACTCATGCGAGGGA	1099
Db	1154	TTACTGTCTATGATTTGTCTTAACAACAACATCTTGATTTCACTCATGTAAGGA	1211
QY	1093	CGGCTTCAAGAGATGAGACCAAGATTTGAAGATTGCTTTTGAATCTGCTTAAGACCTT	1155
Db	1214	CGGCTTCAAGAGATGAGATCTAGATTTGAAGATTGCTTTTGAATCTGCTTAAGACCTT	1271

QY	1153	TCCTATCTTCAAGAAGATGGCAATCCCTAAATCACTTCAACCGGTGATATCAAGCGTTCAAC	1212
Db	1274	TCATATCTTCAAGAAGATGGCAATCCGAAATCACTTCAACCGGTGATATCAAGCGGTCAAC	1333
QY	1213	ATATTGATGATATTTCAAGTTTGAAGCTAAGGTTCTGATTTTGGTCTCTGTCAAGATTGCT	1272
Db	1334	ATATTGATGATATTTCAAGTTTGAAGCTAAGGTTCTGATTTTGGTCTCTGTCAAGATTGCT	1392
QY	1273	TCCTGATCAAAACAGCATGATCAACACGTGTATGGAACTTTGGGTACTTGAGCTTCG	1332
Db	1394	TCCTGATCAAAACAGCATGATCAACACGTGTATGGAACTTTGGGTACTTTGGGTCTCG	1453
QY	1333	GAATACGCTGAAACCGGAAAGCTACACGAGAAAGCTAGCTTTCTCATTTGGGGTGTG	1392
Db	1454	GAATATGCTGAAATGCGAAAGCTACACGAAAGTCTGACGTTTCTCATTTGGGGTGTGTA	1513
QY	1393	CTTTTGAAGCTCATTACTGACGCTGACCCGTTATGSCAAATGTCTATGATGATGAC	1452
Db	1514	CTTTTGAAGCTTATTACTGGGAGCGCGCGCTGTTATGAGAAACATGTCTATGATGATGAC	1573
QY	1453	AGCTTATGTGACTTGGGACCAACCTTGTCTTAAACGAGATTTGACAAAGACCTTTGAG	1512
Db	1574	AGCTTATGTGACTTGGGACCAACCTTGTCTTAAACGAGACATCTTGAGAAAGGAGATTTTGA	1633
QY	1513	GGTTTACCTGATGCAAAAGATGAATTAATGGGATATGACAGAGAGAGATGGCTCGATGGTT	1572
Db	1634	GGTTTGGGTGATTTAAAGATGGGATTAATGATGATGACAGAGAGAGATGGCTCGATGGTT	1693
QY	1573	GCTTGTGCTGCGGCTTGTGTTCGCCATTCAAGCTCGCGACACCTCGCATGAGCCAGATT	1632
Db	1694	GCTTGTGCTGCGGCTTGTGTTCGCCATTCAAGCTCGCGACACCTCGCATGAGCCAGATA	1753
QY	1633	GTCGTCGCGTTAGAAAGAAATGATATCACTGTCGAGATCTTAAACGAAGGATGAGCCAGGT	1692
Db	1754	GTCGTCGCGTTAGAAAGAAATGATATCACTGTCGAGATCTTAAACGAAGGATGAGCCAGGT	1813
QY	1693	CAAAACAATGTATACAGCTCATACGAGGAAGACCCGATTATGATCGAGCCAGATACAAT	1752
Db	1814	CACAGCAACGATATCAGCTCATATGAGGAAGACACAGATATGACAGAGCCATATACAC	1873
QY	1753	GAAGACATGAAAGAACTTTAGAAAATGGCACTTGGAACTCAAGAGTACAAACCGACGGGT	1812
Db	1874	GACACACATGATTAAGTTTAAAGAAAATGGCTCTTGGAACTCAAGAGTACAAACCGGAC	1933
QY	1813	GAGTACAGTATCGCACCGATGATCTAATGAGCTGATACCCGCTGGTTCAACGAGGAGGCG	1872
Db	1934	GAGTACAGTATCCACCACTGATACGAGCTGTACCCGCTGGTTTAAACGAGGAAAGGT	1993
QY	1873	CAAAACAACGCGAAATGAGATGGGGAAGATTAAAGAACCGGTCAAGGTTTATGATGA	1932
Db	1994	CAAGCCACACGAGAAATGAGATGGGGAAGATTAAAGAAAACGGGTCAAGGTTTATGATGA	2053
QY	1933	CCCTTCTCTTAA 1944	
Db	2054	CCCTTCTCTTAA 2065	

RESULT 13			
LOCUS	AY089024	2324 bp	mRNA linear
DEFINITION	Arabidopsis thaliana clone 17909 mRNA, complete sequence.		
ACCESSION	AY089024		
VERSION	AY089024.1	GI:21407798	
KEYWORDS	FLI cDNA.		
SOURCE	Arabidopsis thaliana (thale cress)		
ORGANISM	Arabidopsis thaliana		
	Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.		
REFERENCE	1 (bases 1 to 2324)		
AUTHORS	Haas,B.U., Volkovskiy,N., Town,C.D., Troukhan,M., Alexandrov,N., Feldmann,K.A., Flavell,R.B., White,O. and Salberg,S.L.		
TITLE	Full-length messenger RNA sequences greatly improve genome		



QY 1576 TGTGCTGGCGGCTTGTGTTCCCATTCAGTCTGCGCGAGACCTGGCATGAGCAGATTGTG 1635  
DB 1691 TGGCTCTGACAGTCTGTGTTGCCATTAGCTCTGCGCGAGACCTGGCATGAGCAGATTGTG 1750  
QY 1636 CGTGGCTTGAAGAAATGTTATCACTGTGATCTTTAACGAGGAGTGAAGCAGGTCGA 1695  
DB 1751 CGGGCCGTTGAAGAAATGTTATCGCTGTCTGATCTTTAACGAGGAGTGAAGCAGGTCGA 1810  
QY 1696 AGCAATGTATGAGCTCATTCGAGAGAGACCGATTATGATCTGAGCCAGTACAAATGAA 1755  
DB 1811 AGCAAGGTATGAGCTCATTCGAGAGAGACCGATTATGATCTGAGCCAGTACAAATGAA 1870  
QY 1756 GACATGAAGAAGTTTGAAGAAATGAGCACTTGAACCTCAAGAGTACAGCCAGCGGTGAG 1815  
DB 1871 GACATGAAGAAGTTTGAAGAAATGAGCACTTGAACCTCAAGAGTACAGCCAGCGGTGAG 1930  
QY 1816 TACAGTAATCCGACCGAGTACTATGAGTACTGATCCCTGTGTTCAAGAGCCAGCGGCGAA 1875  
DB 1931 TACAGTAATCCGACCGAGTACTATGAGTACTGATCCCTGTGTTCAAGAGCCAGCGGCGAA 1990  
QY 1876 ACCACCGGGAATGAGATGGGAAAGATTAAAGAAACCGGTGAGGTTATAGTGAAGCT 1935  
DB 1991 GCCACGAGGAATGAGATGGGAAAGATTAAAGAAACCGGTGAGGTTATAGTGAAGCT 2050  
QY 1936 TCTCTTTAA 1944  
DB 2051 TCTCTTTAA 2059

## RESULT 14

AX825736 1515 bp DNA linear PAT 11-DEC-2003  
LOCUS AX825736  
DEFINITION Sequence 34 from Patent WO03072763.  
ACCESSION AX825736  
VERSION AX825736.1 GI:39751253  
KEYWORDS  
SOURCE  
ORGANISM Zea mays  
Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
Clade; Panicoideae; Andropogoneae; Zea.

REFERENCE  
AUTHORS Goring, D., Silva, N. and Haffani, Y.Z.  
TITLE Increasing plant seed production  
JOURNAL Patent: WO 03072763-A 34 04-SEP-2003;  
Goring, Daphne (CA); Silva, Nancy (CA); Haffani, Yousr, Z. (CA)

FEATURES  
source  
1. 1515  
Location/Qualifiers  
/organism="Zea mays"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:4577"

## ORIGIN

Query Match 31.3%; Score 608.4; DB 6; Length 1515;  
Best Local Similarity 68.9%; Pred. No. 8.9e-114;  
Matches 866; Conservative 0; Mismatches 381; Indels 9; Gaps 2;

QY 673 CTTCCACCTCCACACCGCTTTCATGACAGACGCGCGCTCCGACTACTCGAACCT 732  
DB 43 CCACCCACCCACGATGATTAATAGTAGTCGGGATCTGCTTCTATTAATCTCTGGCGGC 102  
QY 733 CCAATCTTCTCCACACCGCTCCAGGCGCTGTGTATAGCTTTTCCAAAGACACTTTTACA 792  
DB 103 GAGATCTTACTCCACCATCTCCCTGGAGCTGTCTTGGCTTCTCGAAGACACATTCACC 162  
QY 793 TACGAGAGCTAGCTAGAGCCACCAATGTGTTTCTCCGAGCGCAATCTGTAGGACAAGGC 852  
DB 163 TACGAGAGCTGTAGAGGCTAGCTAGATGATTTCTCGATCTTAATCTCTTGAACAAGGT 222  
QY 853 GGGTTGGTTAGCTGACAAAGGTGTGCTTCTGAGGAGAAAGATTGCTGTGAAGCAG 912  
DB 223 GGGTTGGTTAGCTGACAAAGGTGTGCTTCTGAGGAGAAAGATTGCTGTGAAGCAG 282

QY 913 TTGAAGTTGGAGTGATGATGAGGAGAGAGGAGATTTCAGGACAGAGTTGATCATGAC 972  
DB 283 TTGAAGTTGGAGTGATGATGAGGAGAGAGGAGATTTCAGGAGTTGATGATCATGAC 342  
QY 973 AGAGTTACCAACAGGATCTGTGTCTCTTGTGTTTATGATCGCGCGTGCACAAAGA 1032  
DB 343 CGAGTACATCAACAAACCTTGTGTCTTGTGTTGCTTATGATCTTGTGAGGACAGAGG 402  
QY 1033 TTGCTGTATGAGTTGTTGTTCTTAAACAATCTGAGCTTCACTCCATGCGAGGGA 1092  
DB 403 CTGCTGTATGAGTTGTTGTTCTTAAACAATCTGAGTTCACTTAAATGAGGAAAGT 462  
QY 1093 CGGCTTCAATGAATGAGGACCAAGTTGAAGTTGCTCTTGATCTGCTAAAGACCTT 1152  
DB 463 CCACCAACATGAGAGTGGCTGCTGATTAAGATCAAGTTGGTGTCTCCAAAGGCTTAA 522  
QY 1153 TCTTATCTTCAATGAAGATGCAATCTTAATCATTCACCGATATCAAGGCTTCAAC 1212  
DB 523 GCTTATCTTCAATGAAGATGCAATCTTAATCATTCACCGATATCAAGGCTTCAAC 582  
QY 1213 AATTTGATGATTTCAAGTTGAAGTTGATGTTGCTGATTTGCTTGTCTAAAGATTGCT 1272  
DB 583 AATTTGATGATTTCAAGTTGAAGTTGATGTTGCTGATTTGCTTGTCTAAAGATTGCT 642  
QY 1273 TCTGATACAAACAGCATGATATCAACAGGTGATGAGAACTTTGGGTACTTGGCTCG 1332  
DB 643 ACTGATACAAACAGCATGATATCAACAGGTGATGAGAACTTTGGGTACTTGGCTCG 702  
QY 1333 GAATGCTGCAAGCGGAAAGCTCAAGGAGATGCTGAGTTTCTCAATTTGGCGTTGG 1392  
DB 703 GAGTATGATCTTCTGCGAGAGCTAACAAAGATCCAGTATTTCTTGGAGATCATG 762  
QY 1393 CTTTGGAGCTCATTAATCTGAGAGCTGACCCGTTGATGCAACAATGCTATGATGATGAC 1452  
DB 763 CTTTGGAGCTCATTAATCTGAGAGCTGACCCGTTGATGCAACAATGCTATGATGATGAC 822  
QY 1453 AGCTTAGTTGATCTGGGACGACCAATGCTTAAACGAGATCTGAGCAAGAGACTTTGAG 1512  
DB 823 AGCTTAGTTGATCTGGGACGACCAATGCTTAAACGAGATCTGAGCAAGAGACTTTGAG 942  
QY 1513 GCTTATGATGATCTGCGGCTGGAAGAGACTTCAATCTTAATGAGATGCAAGATGAT 882  
DB 883 GCTTATGATGATCTGCGGCTGGAAGAGACTTCAATCTTAATGAGATGCAAGATGAT 1572  
QY 1573 GCTTATGATGATCTGCGGCTGGAAGAGACTTCAATCTTAATGAGATGCAAGATGAT 942  
DB 943 GCTTATGATGATCTGCGGCTGGAAGAGACTTCAATCTTAATGAGATGCAAGATGAT 1002  
QY 1633 GTGGCTGCTTGAAGAGAAATGATATCACTGTCAGATCTTAAACGAGAGATGACAGGT 1692  
DB 1003 GTGGCTGCTTGAAGAGAAATGATATCACTGTCAGATCTTAAACGAGAGATGACAGGT 1062  
QY 1693 CAAGCATGTATACAGCTCATACGAGAGACCGATTAATGATCTGAGCAGTAAAT 1752  
DB 1063 CATAGCGCTTCTTGGGTATAC---AGCAGCTCCGATTAATGATCTGAGCAGTAAAT 1119  
QY 1753 GAAGCATGAGAAAGTTTGAAGAAATGACCTTGAACCTCAAGATGACCAACGCGAGT 1812  
DB 1120 GAAGCATGAGAAAGTTTGAAGAAATGACCTTGAACCTCAAGATGACCAACGCGAGT 1173  
QY 1813 GAGTATGATATCGACAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1872  
DB 1174 GAGTATGATATCGACAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1233  
QY 1873 CAACACACGCGAAATGAGATGAGGAGAAATTAAGAGAACCGGTGATGATGATGATGAT 1928  
DB 1234 CAACACACGCGAAATGAGATGAGGAGAAATTAAGAGAACCGGTGATGATGATGATGATGAT 1289

## RESULT 15

AX825737 1488 bp DNA linear PAT 11-DEC-2003

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DEFINITION Sequence 35 from Patent WO03072763.
ACCESSION AX825737
VERSION AX825737.1 GI:39751254
KEYWORDS
SOURCE
ORGANISM Glycine max (soybean)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
REFERENCE
1 Goring, D., Silva, N. and Hafani, Y. Z.
Increasing plant seed production
Patent: WO 0307263-A 35 04-SEP-2003;
Goring, Daphne (CA); Silva, Nancy (CA); Hafani, Yost, Z. (CA)
Location/Qualifiers
FEATURES
source 1..1488
/mol_type="Glycine max"
/db_xref="taxon:3847"

ORIGIN
Query Match 31.1%; Score 605; DB 6; Length 1488;
Best Local Similarity 71.1%; Pred. No. 4,4e-113;
Matches 848; Conservative 0; Mismatches 330; Indels 15; Gaps 3;

QY 755 CAGGGCTTGTGTTAGGCTTCCAAAAGCATTTACATACGAGAGCTAGTAGGCCA 814
DB 1 CAGGAATTTCTATGGGGTCTCTAAGACATTCAGTATGAGAACTTGGACGGCCAA 60
QY 815 CCATGGTTTCTCCGAGGCACTGTTAGACAAAGCGGATTCGTTAGTGACCAAG 874
DB 61 CTATGGCTTCTGATGCAACTCTCTGACAAAGAGATTGGATATGTGACAGAG 120
QY 875 GTGTGTGCTAGTGGGAAAGATTGCTGTAAGCATTTGAAGTTGGAGTGTAGG 934
DB 121 GAATTTCTCCCAACGGCAAGAGGTGCACTGAAGCAATTTGAAGCTGGAAGCGGCAAG 180
QY 935 GAGAGAGGAGTTTCAAGCAGAGTTGATCATCAGAGATTCAACACAGCATCTGG 994
DB 181 GGGAGCTGAATTCAGAGCTGAAGTTGAGATTAATTAAGCCGTGTCATCACAAGACTTTG 240
QY 995 TGTCTCTTTGTTGTTATTCATTCGCGGTCGCAAAAGATTGCTGATAGTTTTC 1054
DB 241 TTTCTTTGTTGATCTGATCACTGAGTCCAGAGCTGCTTTATGATTTGTTTC 300
QY 1055 CTAAACAATCTGAGCTTCACTTCATGCGAGGAGCGGCTTCAATGAATGAGCA 1114
DB 301 CCAACAAACATTTGGAATTCATTTGATGAAAGGAGACCTACATGATTGGCCCA 360
QY 1115 CCAAGTTGAAGATTGCTTTGGATTTGCTAAAGACTTTTATCTTATCATGAAGATTGCA 1174
DB 361 CAAAGCTAAGATTGCTTTAGATCTGTAAGGAGCTGCGGTATCTCATGAAGATTGTC 420
QY 1175 ATCTTAATCATTCACCGTATATCAAGCTTCAACATATTAATTAATTTCAAGTTTG 1234
DB 421 ATCTTAAGATCATCTGATGATATCAAGCTTCAACATCTTCTGATTTTAAGTTTG 480
QY 1235 AAGCTAAGTTGCTGATTTTGGTCTTGTAGATTGCTTCTGATACAAACGCAATGAT 1294
DB 481 AAGCAAGGTTGCAAGTTTCTGTTGCAAAAGTTTCTTGTATGATCAATCTCATGTTT 540
QY 1295 CAACAGTGTGATGGGAACCTTTGGTATTTGGTCCGGAATAGCGTGCAAGCGGAAGC 1354
DB 541 CTACTCGAGTGAATGGGACTTTTGGGTATTTGGCTCCAGAAATATGCTTTAGTGAAGAAC 600
QY 1355 TCACGGAGAAATCTGAGCTTTTCTCATTTGGCGTTGCTTTGGAGCTCATTAATCTGAGC 1414
DB 601 TGACAGACAAATCAGATGTTTCTCTACGAGTCACTGCTCGAGTTAATTAACCGGAGC 660
QY 1415 GTGACCCGTTGATGCGCAACATGCTATATGATGACAGCTTAAGTTGACTGGGCAAGAC 1474
DB 661 GACGGCCCTCGATAAATTAACAACCTTATGAGAGATGTTGATGAGACTGGGCTAGGC 720

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QY 1475 CATTGCTTAACCGAGCATCTGACAAAGAGACTTTGAGGGTTTACGTATGCAAGATGA 1534
DB 721 CTTTGTCTCACAGAGACTTTGGAAGAGATGATTTGATTTATTTATGACCAAGGCTTC 780
QY 1535 ATAAATGGTATTAACAGAGAGAGATGCTCCGATGGTTTCTGTGCTGGGCTTGCTTC 1594
DB 781 AGAATGACTATATCTTAATGAGATGGCACGAATGGGCTTCTGCTGGGCTTGATGATAC 840
QY 1595 GCCATTGACCTGCGGACAGACTCCGATGAGCCAGATTGTGCGTGGTTAGAAAGAAATG 1654
DB 841 GTCATTTGCGAAAGGCTGCAACCAAGATGAGCAAGTTGTCCGCGCTTCGAAGGAGATG 900
QY 1655 TATCATCTGACATCTTAAAGAGGATGAGACCAAGTCAAGCAATGATATACAGCTCAT 1714
DB 901 TCTCTTACAGATCTGAATGAAGGATTAAGACTTGGACACAGCCTATGATATGATTTCTC 960
QY 1715 ACGAGAGAAACCCGATTTTGAAGTGAAGCAATGATGAAGCAATGAAGAAATTTAGGA 1774
DB 961 A--TGAAAGCTCAGATTATGACATGCAAGTGAAGAGAGAGATGAAAGTTTCAAGGA 1017
QY 1775 AATGSCACTTGGAACTCAAGAGTACAAAGCCAGCGGTGATGATCCAGTATCCAGATG 1834
DB 1018 AATGSCATTTGGAACTCAGAGATATGATGCAAGAGTATGATGATGATGATGATGATG 1077
QY 1835 ACTATGACTGTAACCGTCTGTTTCAAGCAGCAGG-----GCCAAACCAACGCGG 1885
DB 1078 AGTATGTTTAAACCATCAGGCTCAAGTATGTAAGACACAGAGCCGCCAAACCAAGGG 1137
QY 1886 AATGAGATGGGAGATTAAGAAACCGGTCAAGGTTTATGTTGACTTTCT 1938
DB 1138 AATGGAATGAGAAAGATGAAG--AACATCAAGTTTCAATGAGATTTCT 1187

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Search completed: November 13, 2004, 09:46:48  
 Job time : 5555 secs







XX Sequence 1944 BP; 464 A; 550 C; 459 G; 471 T; 0 U; 0 Other;  
SQ Query Match 100.0%; Score 1944; DB 4; Length 1944;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1944; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AMGTCTCGGCGCGCTCTCGGCGGAGTGGTGGCCCTCATCTCCACATCAAACTCCACA 60  
DB 1 AMGTCTCGGCGCGCTCTCGGCGGAGTGGTGGCCCTCATCTCCACATCAAACTCCACA 60  
QY 61 ACCACCACTCTCTCTCCAGCTTCGCTCTCTCCAGCAGCACTCTCTCTCTCTCTCTCGCG 120  
DB 61 ACCACCACTCTCTCTCCAGCTTCGCTCTCTCCAGCAGCACTCTCTCTCTCTCTCTCGCG 120  
QY 121 CCATCCACTATTTCGACATCT 180  
DB 121 CCATCCACTATTTCGACATCT 180  
QY 181 CCATCTCCACCACTCTCATCTTACGCGGGATCTCACTCTCTCTCTCTCTCTCTCTCTCTCA 240  
DB 181 CCATCTCCACCACTCTCATCTTACGCGGGATCTCACTCTCTCTCTCTCTCTCTCTCTCTCA 240  
QY 241 CCGGCTCCAACTAGCGCCGGATCTCCACCGGCACTGTATCTCTCTCTCTCTCTCTCTCTCA 300  
DB 241 CCGGCTCCAACTAGCGCCGGATCTCCACCGGCACTGTATCTCTCTCTCTCTCTCTCTCTCA 300  
QY 301 CCACCTTCACTCCAGAGACCACTGTCTCAATCTTCAACGCGAAGAGATCTCTCTCTCTCA 360  
DB 301 CCACCTTCACTCCAGAGACCACTGTCTCAATCTTCAACGCGAAGAGATCTCTCTCTCTCA 360  
QY 361 CCATCT 420  
DB 361 CCATCT 420  
QY 421 GGAATGCGCATCGGAGAGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 480  
DB 421 GGAATGCGCATCGGAGAGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 480  
QY 481 AAGAGAAAG 540  
DB 481 AAGAGAAAG 540  
QY 541 GGTCCCAAGCGGAGAGCTTACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600  
DB 541 GGTCCCAAGCGGAGAGCTTACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600  
QY 601 ACAACCACTCTCAATCA 660  
DB 601 ACAACCACTCTCAATCA 660  
QY 661 CCACGCGCACTCA 720  
DB 661 CCACGCGCACTCA 720  
QY 721 TACTCGGACGCTCGAGTCA 780  
DB 721 TACTCGGACGCTCGAGTCA 780  
QY 781 AGCATTTTCAATATGAG 840  
DB 781 AGCATTTTCAATATGAG 840  
QY 841 TTAGAGCAAGGCGGCTCA 900  
DB 841 TTAGAGCAAGGCGGCTCA 900  
QY 901 GCTGGAAG 960  
DB 901 GCTGGAAG 960  
QY 961 GAGATCATCAGCAGAGATTACCAAGGATCTGTGTCTCTCTCTCTCTCTCTCTCTCTCTCT 1020  
DB 961 GAGATCATCAGCAGAGATTACCAAGGATCTGTGTCTCTCTCTCTCTCTCTCTCTCTCTCT 1020

DB 961 GAGATCATCAGCAGAGATTACCAAGGATCTGTGTCTCTCTCTCTCTCTCTCTCTCTCTCT 1020  
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DB 1021 GGTGCGCAAAAGATTGCTGTCTATGAGAGTGTCTCTCAACAACATCTCGAGCTTCACTCTC 1080  
QY 1081 CATGCGAG 1140  
DB 1081 CATGCGAG 1140  
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QY 1201 AAGGCTTCAACATATGATATGATATTCAGATTGAGAGTAAAGTTGAGTTTGTCTCTT 1260  
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DB 1261 GCTAAGATTGCTTCTGATACAAACACGCACTGATCAACAGTGTATGGAACTTTGGG 1320  
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DB 1321 TACTTGGCTCCGGAATAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380  
QY 1381 TTTGGCGTTGTCTTTTGGAGCTCATTTACTGAGAGTGCACCGGTTATGCCAATATGTC 1440  
DB 1381 TTTGGCGTTGTGTCTTTTGGAGCTCATTTACTGAGAGTGCACCGGTTATGCCAATATGTC 1440  
QY 1441 TATGTAGATGACAGCTTATGTTGACTGGGCAAGCACTTGTATTAACGAGAGATCGAGCA 1500  
DB 1441 TATGTAGATGACAGCTTATGTTGACTGGGCAAGCACTTGTATTAACGAGAGATCGAGCA 1500  
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DB 1501 GGAAGCTTTGAGAGGTTTATGCTGATGCAAGAGATATATGAGATGACAGAGAGAGATG 1560  
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DB 1561 GCTGCGATGCTGTGTGTGTGCTGCGGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1620  
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DB 1621 ATGAGCCAGATTGT 1680  
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DB 1741 AGCCAGTATCAATGAG 1800  
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DB 1861 AGCAGCGAGGCGCAACCAACAGGAAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1920  
QY 1921 GGTATATGATGACCTTCTCTTTAA 1944  
DB 1921 GGTATATGATGACCTTCTCTTTAA 1944

RESULT 2  
ACF36548  
ID ACF36548 standard; cDNA; 1944 BP.  
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AC ACF36548;  
XX

DT 18-DEC-2003 (first entry)  
XX B. napus PERK1 receptor kinase encoding cDNA.  
DE PERK1; transgenic; plant; proline-rich extensin-like receptor kinase;  
XX wound; pathogen resistance; plant growth; seed production; gene; ss.  
OS Brassica napus.  
XX  
FH Key Location/Qualifiers  
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/product= "PERK1"  
/note= "Proline-rich Extensin-like Receptor Kinase"  
XX  
XX WO2003072763-A1.  
XX  
XX 04-SEP-2003.  
XX  
XX 28-FEB-2003; 2003WO-CA000274.  
XX  
XX 28-FEB-2002; 2002CA-02373903.  
XX 28-FEB-2002; 2002US-00086464.  
XX  
XX (GORI/) GORING D.  
XX (SIUV/) SILVA N.  
XX (HAFF/) HAFFANI Y Z.  
XX  
XX Goring D, Silva N, Haffani YZ;  
XX  
XX WPI; 2003-712727/67.  
XX  
XX P-PSDB; ABR82937.  
XX  
XX  
XX Producing a transgenic plant having an increased plant resistance, plant  
XX growth or seed production comprises transforming a plant with a nucleic  
XX acid molecule having a Proline-rich Extensin-like Receptor Kinase  
XX activity.  
XX  
XX  
XX Claim 3; Fig 1A; 123bp, English.  
XX  
XX The invention relates to producing a transgenic plant having increased  
XX plant height, number of branches, number of seed pods and/or seed  
XX production compared to a non-transgenic plant, and/or quicker flowering  
XX or later senescence compared to a non-transgenic plant. The method  
XX involves transforming a plant with a vector including a Proline-rich  
XX Extensin-like Receptor Kinase (PERK) nucleic acid molecule or a nucleic  
XX acid molecule having PERK activity. The method, as well as the PERK  
XX nucleic acid molecule and polypeptide, are useful in increasing plant  
XX resistance to wounding and pathogens and in increasing plant growth and  
XX seed production. The nucleic acid molecule and polypeptide may also be  
XX used in producing transgenic plants or transgenic host cells. The present  
XX sequence represents a cDNA encoding a B. napus PERK1 receptor kinase  
XX polypeptide  
XX  
XX Sequence 1944 BP; 464 A; 550 C; 459 G; 471 T; 0 U; 0 Other;  
XX  
XX Query Match 100.0%; Score 1944; DB 10; Length 1944;  
XX Best Local Similarity 100.0%; Pred. No. 0;  
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DB 361 CCATCT 420  
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DB 661 CCACGCAACCTCTCTCCACCTCTCCACCTCTCCACCTCTCCACCTCTCCACCTCTCC 720  
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DB 721 TACTGGAACGCTTCAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 780  
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DB 841 TTAGGACAAAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 900  
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Db 1861 AGCAGCGAGGCTCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 1920
QY 1921 GGTATATGATGACCTTCTCTTAA 1944
Db 1921 GGTATATGATGACCTTCTCTTAA 1944

RESULT 3
ACF36549
ID ACF36549 standard; cDNA; 2189 BP.
XX ACF36549;
AC 18-DEC-2003 (first entry)
DT
XX
DE B. napus PERK1 receptor kinase encoding cDNA.
XX
KM PERK1; transgenic; plant; proline-rich extensin-like receptor kinase;
KM wound; pathogen resistance; plant growth; seed production; gene; ss.
XX
XX Brassica napus.
OS
XX
FH Key Location/Qualifiers
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FT C
FT /note= "ABR82938; this protein contains the amino acids
FT corresponding to 5' and 3' UTR regions, though only the
FT relevant aa residues (ABR82937) is used in the invention"
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XX
XX 04-SRP-2003.
XX
XX 28-FEB-2003; 2003MO-CA000274.
XX
XX 28-FEB-2002; 2002CA-02373903.
XX
XX 28-FEB-2002; 2002US-00086464.
XX
XX (GORI/) GORING D.
XX (SILV/) SILVA N.
XX (HAFF/) HAFFANI Y Z.
XX
XX Goring D, Silva N, Haffani YZ;
XX
XX WPI: 2003-712727/67.
XX
XX P-PSDB; ABR82937, ABR82938.
XX
XX Producing a transgenic plant having an increased plant resistance, plant
XX growth or seed production comprises transforming a plant with a nucleic
XX acid molecule having a Proline-rich Extensin-like Receptor Kinase
XX activity.
XX
XX Disclosure; Fig 1D; 123pp; English.
XX
XX The invention relates to producing a transgenic plant having increased
XX plant height, number of branches, number of seed pods and/or seed
XX production compared to a non-transgenic plant, and/or quicker flowering
XX or later senescence compared to a non-transgenic plant. The method
XX involves transforming a plant with a vector including a Proline-rich
XX Extensin-like Receptor Kinase (PERK) nucleic acid molecule or a nucleic
XX acid molecule having PERK activity. The method, as well as the PERK
XX nucleic acid molecule and polypeptide, are useful in increasing plant
XX resistance to wounding and pathogens and in increasing plant growth and
XX seed production. The nucleic acid molecule and polypeptide may also be
XX used in producing transgenic plants or transgenic host cells. The present
XX sequence represents a cDNA encoding a B. napus PERK1 receptor kinase
XX polypeptide
XX
XX Sequence 2189 BP; 544 A; 592 C; 494 G; 559 T; 0 U; 0 Other;
XX
XX
XX Query Match 100.0%; Score 1944; DB 10; Length 2189;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 1944; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 157 ACCACCACTCTCTCTGAGCTTCCGCTCTCTCTCTCCACACACCTTTCTCTCCGCG 216
QY 121 CCATCCATATTCGACATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 180
Db 121 CCATCCATATTCGACATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 276
QY 217 CCATCCATATTCGACATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
Db 181 CCATCCATCAACCACTTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 336
QY 277 CCATCTCCACCAACTTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 300
Db 241 CCGGCTCCAACTAGCGCGGATCTCCACCGGACCTGTTACTCTCTCTCTCTCTCTCTCT 396
QY 337 CCGGCTCCAACTAGCGCGGATCTCCACCGGACCTGTTACTCTCTCTCTCTCTCTCTCT 360
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[illegible]

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Qy	1561	GCTGGCATGTTGCTTGCTGCTG	CGGCTTGTTGCTTGC	CATTGAGCTCGCCGAGACTGCG	1620
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ID	ACF36557 standard; DNA, 1959 BP.				
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AC	ACF36557;				
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DT	18-DEC-2003 (first entry)				
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KW	PERK1; transgenic; plant; proline-rich extensin-like receptor kinase;				
KW	wound; pathogen resistance; plant growth; seed production; gene; ds.				
XX					
OS	Arabidopsis thaliana.				
XX					
PN	WO2003072763-A1.				
XX					
PD	04-SEP-2003.				
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PF	28-FEB-2003; 2003WO-CA000274.				
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PR	28-FEB-2002; 2002CA-02373903.				
PR	28-FEB-2002; 2002US-00086464.				
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PA	(GORI/) GORING D.				
PA	(SILV/) SILVA N.				
PA	(HAFV/) HAFFANI Y Z.				
XX					
PI	Goring D, Silva N, Haffani YZ;				
XX					
DR	WPI; 2003-712727/67.				
XX					
PT	Producing a transgenic plant having an increased plant resistance, plant				
PT	growth or seed production comprises transforming a plant with a nucleic				



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XX AAC36968;  
XX 17-OCT-2000 (first entry)  
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KW protein identification; signal transduction pathway; metabolic pathway;  
KW promoter; termination sequence; ss.  
OS Arabidopsis thaliana.  
XX EP1033405-A2.  
XX 06-SEP-2000.  
PD  
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PF  
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PR 23-AUG-1999; 99US-0149930P.  
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PR 01-SEP-1999; 99US-0151930P.  
PR 07-SEP-1999; 99US-0152363P.  
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PR 13-SEP-1999; 99US-0153758P.  
PR 15-SEP-1999; 99US-0154018P.  
PR 16-SEP-1999; 99US-0154039P.  
PR 20-SEP-1999; 99US-0154779P.  
PR 22-SEP-1999; 99US-0155139P.  
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PR 24-SEP-1999; 99US-0155659P.  
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PR 29-SEP-1999; 99US-0156596P.  
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PR 05-OCT-1999; 99US-0157753P.  
PR 06-OCT-1999; 99US-0157865P.  
PR 07-OCT-1999; 99US-0158029P.  
PR 08-OCT-1999; 99US-0158232P.  
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PR 29-OCT-1999; 99US-0162142P.

Query Match 69.0%; Score 1341.2; DB 3; Length 2324;  
Best Local Similarity 82.8%; Pred. No. 8.9e-309;  
Matches 1598; Conservative 0; Mismatches 303; Indels 28; Gaps 5;

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144 TCTCCACCGCTCTCTCCCAAACTCGACACACCATCTCTCTCAGAGCCTCTCT 203  
91 CCTCCCAACACAC-----CTTCTCTCCCGCGCGCATCTACTATTCGAACAT 141  
204 CTTCTCTCCACCAACATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 263  
142 CTTCT 201  
264 CTTCT 323  
QY 202 AGCGCGGATCTCAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 261  
324 A-----CT 371  
262 TCTCCACCGCGCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 321  
372 CCGCGCT 431  
432 CCAACGATCT 491  
382 TCT 441  
492 TCTGATCT 551  
442 GCT 498  
552 GCTATCT 611  
499 GACGAGAAAGTCTTCTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 558  
612 CAGACGATGAAGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 671  
559 CTTTACGTTGAG 618  
672 CTTTACGTTGAG 731  
619 GTCTGAGCT 675  
732 CATGATGAG 791  
676 CCACCTCCACACCGCT 735  
792 CCACTCTCCACACGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 851  
736 GTTCT 795  
852 GTTCT 911  
796 GAGAGCTAGCTAG 855  
912 GAGAGAGTTGTGAAG 971  
856 TTCTGTTAGTGAAG 915  
972 TTCTGTTAGTGAAG 1031  
916 AAAGTTGGAG 975  
1032 AAAGTTGGAG 1091  
976 GTTCAACAGGATCTGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1035  
1092 GTTCAACAGGATCTGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1151  
1036 CTGTCTATGAGTTGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1095  
1152 CTGTCTATGAGTTGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1211  
1096 CTTAAGATGAGATGAG 1155







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QY 1175 ATCCCTAAATCATTCCCGGATATATCAAGGCTTCAACATATTGATAGATTCAAGTTG 1234
Db 421 ATCTTAAGATCATCCATCGGATATCAAAAGCTGCCAACATCCCTTCGATTTTAACTTTG 480
QY 1235 AAGCTAAGGTGGTGGATTTTGGCTTGTCTGCTAAGATGCTTCTGTATACAAACAGCATGTAT 1294
Db 481 AAGCAAGGTGGAGATTTCCGCTTGCCTGCAAGATTTCTTCTGATGCAATACATCATGTTT 540
QY 1295 CAACAGTGTATGGAGAACCTTTGGTACTTGGCTCCGGAATACGCTGCAAGCGGAAGC 1354
Db 541 CTACTGAGATGATGGGAGACTTTTGGGATTTGGCTCCAGAAATATGCTTCTAGTGGAAAC 600
QY 1355 TCACGAGAAAGTGTGACGTTTCTCATTTGGCGGTGTGCTTTGGAGCTCATATTGAC 1414
Db 601 TCACACAAATCATGATGTTTCTCTCAAGATCATGCTCCGAGTTAATTAACCGAG 660
QY 1415 GTCCGACCCGTTGATGCGCAACATGTCTATGTATGATACAGCTTAGTGACTGGGACGAC 1474
Db 661 GACGCGCCCTCATTAATAATCAAACTTTATGAGAGATGTTGGTAGATGGGCTTAAGGC 720
QY 1475 CATTTGCTTAACCGAGCATCTGAGCAAGAGACTTTGAGGCTTTAGCTGATGCAAGATGA 1534
Db 721 CTTTGGCTCACAGAGCTTTGGAAGAGATGATTTGATTTCTATTAATTAAGCCAGGCTCC 780
QY 1535 AATAAGGATGACAGAGAGAGATGGCTCGCATGGTTGCTTGTGCTGCGCTTGTGTTG 1594
Db 781 AATAAGTACTATGATCTTAATGAGATGGACGAATGGTGGCTTCTGCTGCGCTTGCATAC 840
QY 1595 GCCATTACGCTCGCGCAGACTCGCATGAGCCAGATGTGGCGTGTAGAAAGAAAG 1654
Db 841 GTCATTGCGCAAGCTCGACCAAGATAGCCAGTTGTCGCGCTCTCGAAGAGATG 900
QY 1655 TATCACTGCAATCTTTAAAGAGGATGAGACCAAGTCAAAAGCATGTATACAGCTCAT 1714
Db 901 TCTCTTAGCAGATCTGATGAAAGATTAAGACTTGAACAGCACTAATGATAGTTCTC 960
QY 1715 AGGAGAGAGCAACCATTTTGACTGAGCCAGTACATATGAATGAAGATTGAGA 1774
Db 961 A---TGAAAGCTCAGATTATGACATCGACAGTACAAAGAAACATGAAAAAGTTTCAGGA 1017
QY 1775 AATAGCACTTGAAGTCAAGAGTACCAAGCCAGGGTGAATACGTAATCCGACCAAGT 1834
Db 1018 AATAGCACTTGGGAATCTCAGAGATATGTGCAAGCATGATGACATGCGCTTCAAGTG 1077
QY 1835 ACTATGACTGTACCCGCTGTGTTCAAGCAGCGAGG-----GCCAACCACACGCG 1885
Db 1078 AGTATGTTTAAACCATCAGGCTCAAGTATGAGACAGAGCCGCCAACAACAGAGG 1137
QY 1886 AATAGGAGTGGGGAAGATTAAAGAACCGGTCAAGGTTATAGTGACCTTCT 1938
Db 1138 AATGGAATGAGAAAGATGAAG---MACAATCAAGTTCAGTGAAGTTCT 1187

RESULT 8
ACF36554
ID ACF36554 strand, DNA, 1812 BP.
XX ACF36554;
AC ACF36554;
XX
DT 18-DEC-2003 (first entry)
XX
DE O. sativa PERK protein encoding genomic DNA.
XX
KW PERK1; transgenic; plant; proline-rich extensin-like receptor kinase;
KW wound; pathogen resistance; plant growth; seed production; rice; gene;
KW ds.
XX
OS Oryza sativa.
XX
XX WO2003072763-A1.
XX
XX 04-SEP-2003.
XX

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PF 28-FEB-2003; 2003MO-CA000274.
XX
PR 28-FEB-2002; 2002CA-02373903.
PR 28-FEB-2002; 2002US-0006464.
XX
PA (GORI/) GORING D.
PA (SILV/) SILVA N.
PA (HAFF/) HAFANI Y Z.
PI
PI Goring D, Silva N, Haffani YZ;
XX
XX WPI; 2003-712727/67.
XX
XX Producing a transgenic plant having an increased plant resistance, plant
XX growth or seed production comprises transforming a plant with a nucleic
XX acid molecule having a Proline-rich Extensin-like Receptor Kinase
XX activity.
XX
XX Disclosure; Fig 21a; 123bp; English.
XX
XX The invention relates to producing a transgenic plant having increased
XX plant height, number of branches, number of seed pods and/or seed
XX production compared to a non-transgenic plant, and/or quicker flowering
XX or later senescence compared to a non-transgenic plant. The method
XX involves transforming a plant with a vector including a Proline-rich
XX Extensin-like Receptor Kinase (PERK) nucleic acid molecule or a nucleic
XX acid molecule having PERK activity. The method, as well as the PERK
XX nucleic acid molecule and polypeptide, are useful in increasing plant
XX resistance to wounding and pathogens and in increasing plant growth and
XX seed production. The nucleic acid molecule and polypeptide may also be
XX used in producing transgenic plants or transgenic host cells. The present
XX sequence represents an O. sativa PERK protein encoding genomic DNA (TIGR
XX Accession No. TC102111)
SQ
Sequence 1812 BP; 409 A; 487 C; 512 G; 404 T; 0 U; 0 Other;

Query Match 29.1%; Score 566.6; DB 10; Length 1812;
Best Local Similarity 66.7%; Pred. No. 1.8e-124;
Matches 847; Conservative 0; Mismatches 404; Indels 18; Gaps 2;

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Db 382 CCGCGCGCGCGCCGCCGCCCGCGCTTCAAAAGGAGATCACTTAAGTGGGAGTGAACCAAAAT 441
QY 583 TGGCGGCAACAAAGCAACACACCGTCAATGTGTGACGTCATTAACCAACCA 642
Db 442 TGGCAGCAAAATGTGTCCTTCACTTCACTGATCATGTGTGAAGAAGTGCTTGCAT 501
QY 643 CCTAAGGCTCCATCTCCACACGAGCAACCTCTCCACCTCCACCAACCGCTTTCATGAGC 702
Db 502 CCTCCCTCC-----ACCACCTCTGCTCCACTAAATGATACAGTGTGT 546
QY 703 AGCAGCGCGGCTCCGATCTCGACGCGTCCAGTTCTTCTCCACCGCTTCAAGGCTT 762
Db 547 GGTTCGTGCTCAAAATTAATCTCCGCTGCGACCAACCAACCACTCTGTGTGTCACCTGTGT 606
QY 763 GTGTAGGCTTCTCCAAAGACCTTTACATACAGAGACTGACTAGAACCAACCAATGCT 822
Db 607 GCATTGGGTTTTCAGAGTATCTTCACTTATGAGACTTGTACGCGGACCAATGGA 666
QY 823 TTCTCCGAGCGAATCTTGTAGACAGAGCGGCTTGTGTTACGTGCAACAAAGTGTGTTG 882
Db 667 TTCTCCGATGCTAAATCTGCTCGGACAGGCGGCTTTGGGTATGTTTCAAAAGAGTTCTG 726
QY 883 CCTAGTGGAAAGAGTGTCTGTGAAGAGCTTGAAGTTGGAGAGTGTACAGGAGAGAG 942
Db 727 CCGAATGGAGACAGAGTGTGTGAAGCAATGAGAGATGGAGAGGAGGAGCGGT 786
QY 943 GAGTTTCAGGACAGAGTTGAGATCATCAGACAGTTTCAACCAAGGATGTGTTCTTT 1002
Db 787 GAATTTCAAGGCGGAGAGTTGAGATTTATCAGCGGATACATCAAGAGATTTTGAACATTG 846
QY 1003 GTTGGTTATGTCATGCGCGGTGCCAAAGAGTTGTTGCTATGAGTTGTTCTTAACAAC 1062

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QY      1343 CAGCGGAAAGCTCAGGAGAACTGACGTTTCTCATTTGGCGTGTGCTTTGGACC 1402
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QY      1403 TCATTAAGTGCAGCGGCGGTTGATGCCAACAATGTCATATGATGACGTTAGTTG 1462
      |||
      487 TTTATTGCGGGCGGAAACCTGTTGACCAATCTCAGCCCTTANGTGAAAGCGCTGGTG 546
QY      1463 ACTGGGACGACCATTCCTTAAACGAGCATCTGAGCAGAGACCTTGAAGGTTTACGTG 1522
      |||
      547 AATGGGCTGACACTTGGCTTACTCAAGCACTTGAGACTGAAATTTGAAGATATAGTGA 606
QY      1523 ATGCAAGATGAATATGGGTATGACAGAGAGAGATGCGTGCATGTTGCTTGTGCTG 1582
      |||
      607 ATCCCTAGGCTTGAAAGAACTTGTGCGAGTGATGTTCCGATGATTAAGCAGCTG 666
QY      1583 CGGCTGTGTCGCCATTC 1601
      |||
      667 CAGCTTGTGTCAGTCATTC 685
Db
RESULT 10
AAC46629
ID      AAC46629 standard; DNA; 1703 BP.
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AC      AAC46629;
XX
DT      18-OCT-2000 (first entry)
XX
DE      Zea mays DNA fragment SEQ ID NO: 50839.
XX
KM      Hybridisation assay; genetic mapping; gene expression control;
KW      protein identification; signal transduction pathway; metabolic; pathway;
XX      promoter; termination sequence; corn; ss.
XX
OS      Zea mays subsp. mays.
XX
PN      EP1033405-A2.
XX
PD      06-SEP-2000.
XX
PF      25-FEB-2000; 2000EP-00301439.
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PR      27-MAY-1999; 99US-0136392P.
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PR 07-SEP-1999; 99US-0152363P.  
PR 10-SEP-1999; 99US-0153070P.  
PR 13-SEP-1999; 99US-0153758P.  
PR 15-SEP-1999; 99US-0154018P.  
PR 16-SEP-1999; 99US-0154039P.  
PR 20-SEP-1999; 99US-0154779P.  
PR 22-SEP-1999; 99US-0155139P.  
PR 23-SEP-1999; 99US-0155486P.  
PR 24-SEP-1999; 99US-0155659P.  
PR 28-SEP-1999; 99US-0156458P.  
PR 29-SEP-1999; 99US-0156596P.  
PR 04-OCT-1999; 99US-0157117P.  
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PR 07-OCT-1999; 99US-0158028P.  
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PR 28-OCT-1999; 99US-0161993P.  
PR 29-OCT-1999; 99US-0162142P.

Query Match 11.4%; Score 215.8; DB 3; Length 1703;  
Best Local Similarity 59.0%; Pred. No. 5.6e-41;  
Matches 430; Conservative 0; Mismatches 287; Indels 12; Gaps 3;

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QY 829 GAGCGCACTTGTAGACAAAGCGGCTGCTTACCTGCAAAAGTG--TGTTCCT 885  
| | | | |  
DB 269 CCCAGTCTTCCTCGGAGAGGAGGTTTGGAGTGTTTTACAAAGGCGGCTTGAAGC 328  
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QY 886 AGTGGAAAGAGTGTCTGAGACACTTGAAGTTGAGAGTGTCTGAGAGAGGAG 945  
| | | | |  
DB 329 ACAGGCCAGGTTGTCTATAAGCAGCTTAAAGGATGGGCTTCAAGAAAGAGAA 388  
| | | | |  
QY 946 TTTCAGCAGAGTTGAGATCATCAGACAGTTACAGCAGCATCTGTCTTGT 1005  
| | | | |  
DB 389 TTCTAGTAGAAGTCTTCATGCTCAGTTACTACATCATCAAACTGTATTTGATT 448  
| | | | |  
QY 1006 GGTATTGCAATCGCGGTGCGCAAAAGATTGCTGTATGATGATTGTTCTTACACAAAT 1065  
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DB 449 GGTATTGTGCTGATAGAGACAGAGACTTCTTTATGAAATATATGCTTGTGATCA 508  
| | | | |  
QY 1066 CTGAGCTTCACTCCATGCGAGGAGAGCGGCTTA-----CAATGATAGACACCA 1119  
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DB 509 CTGAAATCATTTTGACGATCTACCTTGTATTAAGAGCGCTTGGACTGGAACACAGG 568  
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QY 1120 TTGAAGATTGCTTGGATCTGCTAAAGACTTCTTATCTTCATGAAATTGCAATCT 1179  
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DB 569 ATGAAATTTGACAGAGTGTCTGCCAAGAGCTGAGATCTTCAATGCAAAAGCTAATCA 628  
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QY 1180 AAATTCATTCACCGTGAATCAAGGCTTCAAAATATGATGATTTCAAGTTGAAGCT 1239  
| | | | |  
DB 629 CCACTTATTTATAGGATTTCAAGTCAATGCAAGCAATTTGTTGATGAAGTTTCCACCG 688  
| | | | |  
QY 1240 AAGTTGCTGATTTTGTCTTGTCTTGAATGCTTCTGATACAAACA---CGCATGTATCA 1296  
| | | | |  
DB 689 AAGCTGTCTGATTTTGAAGCTTGAAGTGGGTCCAGTTGCGCAAAATCAGTCTCA 748  
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QY 1297 ACACGTGATGGGAACCTTGGTACTTGGCTCGGAATACGCTGCAAGGGAAGGCTC 1356  
| | | | |  
DB 749 ACACGTGATGAGGTATGATATGTTATTTGTCACACAGATATGCTATGACAGGCACTG 808  
| | | | |  
QY 1357 ACAGGAAGTCTGACGTTTCTCATTTGGCGTTTGGCTTTTGGAGCTTACTGAGCGT 1416  
| | | | |  
DB 809 ACAGTGAAGTCTGACGTTATGTTTGGGTTGTCTTGTAGAGTTGATTTAGCGCGT 868  
| | | | |  
QY 1417 CGACCCGTTGATGCAACAATGTCTATGATGATGACGCTTAGTTGATGGGCAAGACA 1476  
| | | | |  
DB 869 AGGCTATTTGACACACACACACACATGAGAACAAATCTTGTCTATGGGCAAGTCT 928  
| | | | |  
QY 1477 TTGCTTAAAC 1485  
| | | | |  
DB 929 CTGTTTAAAC 937  
| | | | |  
RESULT 11  
AAC43029 ID AAC43029 standard; DNA; 1419 BP.  
XX AAC43029;  
AC 17-OCT-2000 (first entry)  
XX Arabidopsis thaliana DNA fragment SEQ ID NO: 37767.  
XX

KM Hybridisation assay; genetic mapping; gene expression control;  
KM protein identification; signal transduction pathway; metabolic pathway;  
KM promoter; termination sequence; ss.  
XX Arabidopsis thaliana.  
OS EPI033405-A2.  
XX  
XX  
PD 06-SEP-2000.  
XX  
PF 25-FEB-2000; 2000EP-00301439.  
XX  
PR 25-FEB-1999; 99US-0121825P.  
PR 05-MAR-1999; 99US-0123180P.  
PR 09-MAR-1999; 99US-0123548P.  
PR 23-MAR-1999; 99US-0125788P.  
PR 25-MAR-1999; 99US-0126264P.  
PR 29-MAR-1999; 99US-0126785P.  
PR 01-APR-1999; 99US-0127462P.  
PR 06-APR-1999; 99US-0128234P.  
PR 08-APR-1999; 99US-0128714P.  
PR 16-APR-1999; 99US-0129845P.  
PR 19-APR-1999; 99US-0130077P.  
PR 21-APR-1999; 99US-0130449P.  
PR 23-APR-1999; 99US-0130510P.  
PR 23-APR-1999; 99US-0130891P.  
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PR 14-MAY-1999; 99US-0134256P.  
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PR 14-MAY-1999; 99US-0134370P.  
PR 18-MAY-1999; 99US-0134768P.  
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PR 24-MAY-1999; 99US-0135629P.  
PR 25-MAY-1999; 99US-0136021P.  
PR 27-MAY-1999; 99US-0136392P.  
PR 28-MAY-1999; 99US-0136782P.  
PR 01-JUN-1999; 99US-0137222P.  
PR 03-JUN-1999; 99US-0137528P.  
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PR 18-JUN-1999; 99US-0139456P.  
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PR 18-JUN-1999; 99US-0139461P.  
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PR 23-JUN-1999; 99US-0140353P.  
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PR 24-JUN-1999; 99US-0140695P.  
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PR 29-JUN-1999; 99US-0140991P.  
PR 30-JUN-1999; 99US-0141287P.  
PR 01-JUL-1999; 99US-0141842P.  
PR 01-JUL-1999; 99US-0142154P.  
PR 02-JUL-1999; 99US-0142055P.  
PR 06-JUL-1999; 99US-0142390P.  
PR 08-JUL-1999; 99US-0142803P.  
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PR 17-AUG-1999; 99US-0149175P.  
PR 18-AUG-1999; 99US-0149466P.  
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PR 27-AUG-1999; 99US-0151065P.  
PR 27-AUG-1999; 99US-0151065P.  
PR 27-AUG-1999; 99US-0151080P.  
PR 30-AUG-1999; 99US-0151303P.  
PR 31-AUG-1999; 99US-0151438P.



PR 01-SEP-1999; 99US-0151930P.  
 PR 07-SEP-1999; 99US-0152363P.  
 PR 10-SEP-1999; 99US-0153070P.  
 PR 13-SEP-1999; 99US-0153758P.  
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 PR 24-SEP-1999; 99US-0155659P.  
 PR 28-SEP-1999; 99US-0156458P.  
 PR 29-SEP-1999; 99US-0156596P.  
 PR 04-OCT-1999; 99US-0157117P.  
 PR 05-OCT-1999; 99US-0157753P.  
 PR 06-OCT-1999; 99US-0157865P.  
 PR 07-OCT-1999; 99US-0158029P.  
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 PR 14-OCT-1999; 99US-0159638P.  
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 PR 21-OCT-1999; 99US-0160767P.  
 PR 21-OCT-1999; 99US-0160768P.  
 PR 21-OCT-1999; 99US-0160770P.  
 PR 21-OCT-1999; 99US-0160814P.  
 PR 21-OCT-1999; 99US-0160815P.  
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 PR 22-OCT-1999; 99US-0160981P.  
 PR 22-OCT-1999; 99US-0161044P.  
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 PR 25-OCT-1999; 99US-0161406P.  
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 PR 26-OCT-1999; 99US-0161360P.  
 PR 26-OCT-1999; 99US-0161361P.  
 PR 28-OCT-1999; 99US-0161920P.  
 PR 28-OCT-1999; 99US-0161922P.  
 PR 28-OCT-1999; 99US-0161933P.  
 PR 29-OCT-1999; 99US-0162142P.

Query Match 10.5%; Score 204.6; DB 3; Length 1419;  
 Best Local Similarity 57.2%; Pred. No. 2,4e-36;  
 Matches 394; Conservative 0; Mismatches 289; Indels 6; Gaps 1;

QY 799 GAGCTAGCTAGAGCGACCAATGTTCTCGAGGCGCAACTGTTAGCAAGGCGGCTC 858  
 DB 436 GAGCTTAGAGCGGCGACGAATGGGCTTTGTAAGAGATGTAAATCGGAAGAGGTTAC 495  
 QY 859 GGTACGTGCAAAAGGCTGTGCTAGTGGAAAGTGTGTGAAGCAAGTTGAA 918  
 DB 496 GGGATTGTGATCGTGCAATTTTAAGTGAACCAAGTCCGCGTCAGAACTTCTT 555  
 QY 919 GTTGGAGGTGTGTCAGGAGAGAGGAGTTTCAGGAGGTTGATGATCAGCAGCTT 978  
 DB 556 AACAAATAGGGGTCAAGAGAGAGAAATTCAAATAGAGGAAAGTTCATTGGCGAGTA 615  
 QY 979 CACACAGGATCTGGGTCTCTTGTGTATTCAGCGCGGTGCAAAAGTTGCTT 1038  
 DB 616 CGACACAGAAATCTTTAGGCTTTAGGGATTGCGGAGGATGATTCAGGATGCTC 675  
 QY 1039 GTCTATGAGTTGTTCTTAACCAATCTCGAGC-----TTCACTTCATGGCGAGGGA 1092  
 DB 676 GTGATACCTTTGTCGCAATGTGTAATTTGAGCAATGATTCAGGATGTTGGGAT 735  
 QY 1093 CGGCTTCAATGGAATGAGCAGCAAGTTGAAGATTGCTTGGATCTGCTAAAGACTT 1152

DB 726 GTCAGCCGCTAAGTGGATATAGTATGATATTAATCTGGGGATGCCAAGGATTG 795  
 QY 1153 TCTTATCTTCAATGAGATGCAATCTTAATCATTCACCGGATATCAAGCTTCAAC 1212  
 DB 796 GCGTATCTACAGAGGCTTTGAGCCAAAGTTGTTACCGGATATTAATCAAGCAAT 855  
 QY 1213 ATATTGATGATTTCAAGTTGAAGCTAAGTTGCTGATTTTGTCTGCTAAGATTGCT 1272  
 DB 856 ATCTTACTTGAATGCCAATGGAATGTAAGTTGCGATTTTGAATGCTTAAGCTTTG 915  
 QY 1273 TCTGATACAAACAGATGATATCAACAGTGGATGGAAGCTTTGGGACTTGGCTCG 1332  
 DB 916 GGGTCTGAGAGAGATTATGTAATCTCGTGTGATGGAACTTTGCTTATGAGACCA 975  
 QY 1333 GATAAGCTGCAAGCGGAAAGCTCAAGAGAGTCAAGCTTTTCATTTGGCGCTTGTG 1392  
 DB 976 GAAATAGCTTGACCGGATGTTAAAGAAAGATGATATGATAGCTCGAATACGTA 1035  
 QY 1393 CTTTGGAGCTCATTAATGAGAGTCAAGCTTGTATGCCAATGCTATATGATGAC 1452  
 DB 1036 ATCATGAGATATATCATCTGGAAGAAACCGGTTGATTATGTCGGCTCAAGAGACCA 1095  
 QY 1453 AGCTTAGTTGACTGGGCGACAGCAACATTGCT 1481  
 DB 1096 ATCTATGGAATGGCTTAATCATGCT 1124

RESULT 12  
 ABZ13121  
 ID ABZ13121 standard; DNA; 1419 BP.

XX ABZ13121;  
 XX 21-JAN-2003 (first entry)  
 XX Arabidopsis thaliana stress regulated gene SEQ ID NO 926.  
 DE Arabidopsis thaliana stress regulated gene SEQ ID NO 926.  
 XX Arabidopsis thaliana; plant; gene; stress; transgenic; ds.  
 XX Arabidopsis thaliana.  
 OS Arabidopsis thaliana.  
 XX MO200216655-A2.  
 XX 28-FEB-2002.  
 PD 24-AUG-2001; 2001MO-US026685.  
 PF 24-AUG-2001; 2000US-0227666P.  
 PR 26-JAN-2001; 2001US-0264647P.  
 PR 22-JUN-2001; 2001US-0300111P.

XX (SCRI ) SCRIIPS RES INST.  
 PA (SYGN ) SYNGENIA PARTICIPATIONS AG.

XX Harper JF, Kreps J, Wang X, Zhu T;  
 PT WPI; 2002-304127/34.

PT Identifying a stress condition to which a plant cell has been exposed and  
 PT producing plants with increased tolerance to these abiotic stresses.  
 XX Claim 144; SEQ ID NO 926; 577BP + Sequence Listing; English.

XX The invention relates to identifying a stress condition to which a plant  
 CC cell has been exposed, comprising: (a) contacting nucleic acid  
 CC representative of expressed polynucleotides in the plant cell with an  
 CC array or probes representative of the plant cell genome; and (b)  
 CC detecting a profile of expressed polynucleotides in the plant cell  
 CC characteristic of a stress response. The method is useful in the  
 CC production of transgenic plants, cells and seeds and in producing plants  
 CC with increased tolerance to abiotic stresses. The present sequence is that  
 CC of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used  
 CC in methods of the invention. Note: The sequence data for this patent is

CC not represented in the printed specification but is based on sequence  
 CC information supplied to Derwent by the European Patent Office  
 XX  
 SQ Sequence 1419 BP, 387 A; 272 C; 401 G; 359 T; 0 U; 0 Other;

Query Match 10.5%; Score 204.6; DB 6; Length 1419;  
 Best Local Similarity 57.2%; Pred. No. 2,4e-38;  
 Matches 394; Conservative 0; Mismatches 289; Indels 6; Gaps 1;

QY 799 GAGCTAGCTAGAGCCCAATGTTCTCCGAGCGCACTTGTAGACAAAGCGGGTTC 858  
 DB 436 GAGCTTGAAGCGGCGCCCAATGCGCTTTGTGAAGGAATGTATCGGAAGGTGTTAC 495  
 QY 859 GGTACGTGCACAAAGGTGTGTGCTTAGTGGGAAAGATGTTGTGAAGCAGTTGAA 918  
 DB 496 GGGATTGTGTATCGGCGATTCTTAAGTGAACCAAGTCCGCTCAAGAACTTGCTT 555  
 QY 919 GTTGGAGTGTGCAGGAGAGAGAGATTTCAGCAGAGGTTGAGATCATCAGCAGACT 978  
 DB 556 AACCAATAGGGGTCAAGCAGAGAGAAATTCAAAGTGAAGTGAAGTCAATGGCGAGTA 615  
 QY 979 CACCACAGGCATCTGTGTCTCTTGTGTGTTATTCATCGCCGCGCAAAAGATTGCTT 1038  
 DB 616 CGACACAAAGATCTTGTATAGGCTTTTAGGCTATTCCGTGAAGGTCATCAGAGTCTC 675  
 QY 1039 GTCTATGAGTTTGTCTTCAACAACATCTCAGC-----TTACCTTCATGCGCAGGGA 1092  
 DB 676 GTGTATGACTTTTGCACAAATGTATTTGAGAGCATGATTCACGGTATGTGGCGAT 735  
 QY 1093 CGGCGCTAACATGGAATGAGACCCAGATTGGAATGCTGTGATCTGCTTAAAGACTT 1152  
 DB 736 GTCAAGCCGCTAACTTGGGATTAACGTAATGAAATATTAATCTGGGGATGCCAAGGATTG 795  
 QY 1153 TCTTATCTTCAATGAGATTTGAATCTTAAATCATTCACCGTATATCAAGGCTTCAAC 1212  
 DB 796 GCGATCTACACGAGGGCTTGAAGCAAAAGTGTTCATCCGGAATTAATCAAGCAAT 855  
 QY 1213 ATATTGATGATTTCAAGTTGAAGCTTAAAGTTGCTGATTTTGTCTTGAAGATTGCT 1272  
 DB 856 ATCTTACTTGAATCGCAATGGAATGCTAAAGTTTGGATTTTGGACTTGTAAAGTCTTG 915  
 QY 1273 TCTGATCAACACAGCAGTATCAACAGCTGATGAGGAACCTTGGTACTTGCTCCG 1332  
 DB 916 GGGTCTGAGACAGTTATTAATCTACTCTGTGATGGAACCTTGGTATGATGACCA 975  
 QY 1333 GAATACGCTGCAGAGGAAAGCTCAGGAAAGTCTGACGTTTCTCATTTGGCGTTGTG 1392  
 DB 976 GAATACGCTTGCACCGGAATGTAAACGAAGAGTGTATCTATAGCTTGGAACTACTA 1035  
 QY 1393 CTTTGGAGCTCAATTAAGTGAAGTGCACCGCTTGTATGCAACAAATGTCTATAGATGAC 1452  
 DB 1036 ATCATGAGATTAATCACTGGAAGAAACCGGTGATTAATAGTGGCTCAAGAGAGACA 1095  
 QY 1453 AGCTTAGTGAAGTGGGACGACCACTTGT 1481  
 DB 1096 AATCTAGTGAATGGCTTAAATCAATGGT 1124

RESULT 13  
 ADN72798  
 ID ADN72798 standard; cDNA, 1161 BP.  
 XX ADN72798;  
 AC  
 XX  
 DT 15-JUL-2004 (first entry)  
 XX  
 DE Thale cress cDNA upregulated in E2Fa/Dpa expressing plants Segid 693.  
 XX  
 KW gene; ss; plant; transgenic; E2Fa/Dpa transcription factor;  
 KW growth regulator; animal feed product; thale cress;  
 KW cell wall biosynthesis; nitrogen metabolism; carbon metabolism.  
 XX  
 OS Arabidopsis thaliana.

XX  
 EN WO2004035798-A2.  
 XX  
 XX 29-APR-2004.  
 PD  
 XX  
 PF 20-OCT-2003; 2003WO-EP011658.  
 XX  
 XX 18-OCT-2002; 2002EP-00079408.  
 XX  
 PA (CROP-) CROPEDESIGN NV.  
 PI Inze D, De Veylder L, Vlieghe K,  
 XX  
 DR WPI; 2004-348466/32.  
 DR P-PSDB; ADN72799.  
 XX  
 PT Altering plant characteristics, useful for producing plants for enzyme or  
 PT pharmaceutical production comprises modifying in a plant, expression of  
 PT one or more nucleic acids and/or modifying level or activity of one or  
 PT more proteins.  
 XX  
 PS Claim 1; SEQ ID NO 693; 134pp; English.  
 XX  
 CC This invention relates to a novel method for altering one or more plant  
 CC characteristics. Specifically, it refers to identifying genes that are up  
 CC - or down-regulated in transgenic plants overexpressing the heterodimeric  
 CC E2Fa/Dpa transcription factor of Arabidopsis and using these sequences to  
 CC alter plant characteristics accordingly. The present invention describes  
 CC generating transgenic plants for the production of growth regulators,  
 CC enzymes, therapeutics, pharmaceuticals and animal feed products, where  
 CC the altered plant characteristics are selected from increased yield or  
 CC biomass, enhanced survival capacity, stress tolerance, plant architecture  
 CC or physiology, altered endoreduplication, biochemistry, signal  
 CC transduction, storage lipid mobilization and/or altered photosynthesis,  
 CC each relative to the corresponding wild type plants. Accordingly, these  
 CC sequences can also be useful as positive or negative selectable markers  
 CC during transformation of cells or tissues. The identified genes play a  
 CC role in a variety of biological processes such as DNA replication, cell  
 CC wall biosynthesis, nitrogen and/or carbon metabolism or they function as  
 CC transcription factors. This polynucleotide sequence is thale cress cDNA  
 CC upregulated 1.3 fold or more in plants overexpressing the E2Fa/Dpa  
 CC transcription factor, given in an exemplification of the invention.  
 XX  
 SQ Sequence 1161 BP; 297 A; 216 C; 328 G; 320 T; 0 U; 0 Other;

Query Match 10.3%; Score 201.2; DB 12; Length 1161;  
 Best Local Similarity 58.5%; Pred. No. 1.5e-37;  
 Matches 372; Conservative 0; Mismatches 258; Indels 6; Gaps 1;

QY 799 GAGCTAGCTAGAGCCCAATGTTCTCCGAGCGAACTTGTAGACAAAGCGGGTTC 858  
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 QY 859 GGTACGTGCACAAAGGTGTGTGCTTAGTGGGAAAGATGTTCTGTGAAGCAGTTGAA 918  
 DB 496 GGGATTGTGTATCGGCGATTCTTAATCTGATGAACCAAGTCCGCTCAAGAACTTGTCT 555  
 QY 919 GTTGGAGTGTGCAGGAGAGAGAGAGTTCAGGACAGAGTTGAGATCATCAGAGATT 978  
 DB 556 AACCAATAGGGGTCAAGCAGAGAGAAATTCAAAGTGAAGTGAAGTCAATTTGGCGAGTA 615  
 QY 979 CACCACAGGCATCTGTGTCTCTTGTGTGTTATTCATCGCCGCTGCCAAGAAAGATTGCTT 1038  
 DB 616 CGACACAAAGATCTTGTATAGGCTTTTAGGCTATTCCGTGAAGGTCATACAGATGCTC 675  
 QY 1039 GTCTATGAGTTTGTCTTCAACAACATCTCAGC-----TTACCTTCATGCGCAGGGA 1092  
 DB 676 GTGTATGACTTTTGCACAAATGTATTTGAGAGCAATGATTCAGGATGTGTCGAT 735  
 QY 1093 CGGCGCTCAATGGAATGAGACCAAGATTGAAGATGCTTGTGATCTGTAAAGACTT 1152  
 DB 736 GTCAAGCCGCTAACTTGGGATTAATGATTAATTAATCTCGGGATGCGCAAGGATTG 795



PR 23-MAR-1999; 99US-0125788P.  
PR 25-MAR-1999; 99US-0126264P.  
PR 29-MAR-1999; 99US-0126785P.  
PR 01-APR-1999; 99US-0127462P.  
PR 06-APR-1999; 99US-0128234P.  
PR 08-APR-1999; 99US-0128714P.  
PR 16-APR-1999; 99US-0129845P.  
PR 19-APR-1999; 99US-0130077P.  
PR 21-APR-1999; 99US-0130443P.  
PR 23-APR-1999; 99US-0130510P.  
PR 23-APR-1999; 99US-0130891P.  
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GenCore version 5.1.6  
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
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and is derived by analysis of the total score distribution.

## SUMMARIES

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; Publication No. US20020199218A1  
; GENERAL INFORMATION:  
; APPLICANT: GORING, Daphne R. et al.  
; TITLE OF INVENTION: PROLINE-RICH EXTENSIN-LIKE RECEPTOR KINASES  
; FILE REFERENCE: P 25,762-A USA  
; CURRENT APPLICATION NUMBER: US/10/086,464  
; PRIOR FILING DATE: 2002-02-28  
; PRIOR APPLICATION NUMBER: US 10/069,304  
; PRIOR FILING DATE: 2002-02-19  
; PRIOR APPLICATION NUMBER: PCT/CA00/00966  
; PRIOR FILING DATE: 2000-08-18  
; PRIOR APPLICATION NUMBER: US 60/149,466  
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; PRIOR APPLICATION NUMBER: US 60/159,122  
; PRIOR FILING DATE: 1999-10-13  
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QY 1321 TACTTGGCTCCGGAATACGCTGCAAGGAGAAAGCTCAGAGAGAGAGTCTGAGCTTTCTCA 1380  
Db 1321 TACTTGGCTCCGGAATACGCTGCAAGGAGAAAGCTCAGAGAGAGAGTCTGAGCTTTCTCA 1380  
QY 1381 TTTGGCGTTGTGCTTTTGGAGCTCATCTACTGAGAGTGAACCCGTTGATGCAATATGTC 1440  
Db 1381 TTTGGCGTTGTGCTTTTGGAGCTCATCTACTGAGAGTGAACCCGTTGATGCAATATGTC 1440  
QY 1441 TATGTAGATGACAGCTTATGTTGACTGGGACAGACATTCCTTAAACGAGATCTGACCA 1500  
Db 1441 TATGTAGATGACAGCTTATGTTGACTGGGACAGACATTCCTTAAACGAGATCTGACCA 1500  
QY 1501 GGAAGACTTGAAGGTTTATGCTGATGCAAAAGATGAAATGGGATATGACAGAGAGATG 1560  
Db 1501 GGAAGACTTGAAGGTTTATGCTGATGCAAAAGATGAAATGGGATATGACAGAGAGATG 1560  
QY 1561 GGTGCGATGTTGCTTGTGTGCTGCGGCTTGTGTGCGCATTCAGCTCGCGGAGACTGCG 1620  
Db 1561 GGTGCGATGTTGCTTGTGTGCTGCGGCTTGTGTGCGCATTCAGCTCGCGGAGACTGCG 1620  
QY 1621 ATGAGCCAAATTTGGTGGTGTGTAAGAGAAATGATCATCTGTCAGTCTTTAAAGAGGG 1680  
Db 1621 ATGAGCCAAATTTGGTGGTGTGTAAGAGAAATGATCATCTGTCAGTCTTTAAAGAGGG 1680  
QY 1681 ATGAGACCAAGGTCNAAGCAATGATACAGCTCATACGAGAGAGAGAGAGAGAGAGAG 1740  
Db 1681 ATGAGACCAAGGTCNAAGCAATGATACAGCTCATACGAGAGAGAGAGAGAGAGAGAG 1740  
QY 1741 AGCCAGTACATGAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1800  
Db 1741 AGCCAGTACATGAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1800  
QY 1801 AAGGCCAGGAGTGAAGTATCCGACCATGATCTATGATCTGATCCGCTGTGTTCA 1860  
Db 1801 AAGGCCAGGAGTGAAGTATCCGACCATGATCTATGATCTGATCCGCTGTGTTCA 1860  
QY 1861 AGCAGGAGAGGAGCAACCAACAGCGAAATGAGATGGGAGAGATTAAGAGAGAGAGAG 1920  
Db 1861 AGCAGGAGAGGAGCAACCAACAGCGAAATGAGATGGGAGAGATTAAGAGAGAGAGAG 1920  
QY 1921 GGTATATGAGACCTTCTCTTTAA 1944  
Db 1921 GGTATATGAGACCTTCTCTTTAA 1944

RESULT 2  
US-10-086-464-3  
; Sequence 3, Application US/10086464  
; Publication No. US20020199218A1  
; GENERAL INFORMATION:  
; APPLICANT: GORING, Daphne R. et al.  
; TITLE OF INVENTION: PROLINE-RICH EXTENSIN-LIKE RECEPTOR KINASES  
; FILE REFERENCE: P 25,762-A USA  
; CURRENT APPLICATION NUMBER: US/10/086,464  
; PRIOR FILING DATE: 2002-02-28  
; PRIOR APPLICATION NUMBER: US 10/069,304  
; PRIOR FILING DATE: 2002-02-19  
; PRIOR APPLICATION NUMBER: PCT/CA00/00966  
; PRIOR FILING DATE: 2000-08-18  
; PRIOR APPLICATION NUMBER: US 60/149,466



PRIOR FILING DATE: 1999-08-19  
PRIOR APPLICATION NUMBER: US 60/159,122  
PRIOR FILING DATE: 1999-10-13  
NUMBER OF SEQ ID NOS: 27  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 3  
LENGTH: 2189  
TYPE: DNA  
ORGANISM: Brassica napus  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)..(2189)  
OTHER INFORMATION:  
US-10-069-464-3

Query Match 100.0%; Score 1944; DB 13; Length 2189;  
Best Local Similarity 100.0%; Pred.No. 0;  
Matches 1944; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTCTCGAGCGGCTCTCGGAGGAGTGGTTCGCTCCATCTCCACATCAAACTCCAGA 60  
DB 97 ATGTCTCGAGCGGCTCTCGGAGGAGTGGTTCGCTCCATCTCCACATCAAACTCCAGA 156  
QY 61 ACCAGCACTCTCTCTCAAGTTCGCTCTCTCTCCACACACACTTCTCTCTCCGCG 120  
DB 157 ACCAGCACTCTCTCTCAAGTTCGCTCTCTCTCCACACACACTTCTCTCTCCGCG 216  
QY 121 CCATCCACTATTCGAGCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 180  
DB 217 CCATCCACTATTCGAGCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 276  
QY 181 CCATCTCCACCACTCCATCTAGCGCGAGATCTCACTCTCTCTCTCTCTCTCTCTCTCA 240  
DB 277 CCATCTCCACCACTCCATCTAGCGCGAGATCTCACTCTCTCTCTCTCTCTCTCTCTCA 336  
QY 241 CCGGCTCCAACTACGCGCGAGATCTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 300  
DB 337 CCGGCTCCAACTACGCGCGAGATCTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 396  
QY 301 CCACCTTCACTCCAGAGACCAAGGATCTCACTCTCTCTCTCTCTCTCTCTCTCTCTCT 360  
DB 397 CCACCTTCACTCCAGAGACCAAGGATCTCACTCTCTCTCTCTCTCTCTCTCTCTCTCT 456  
QY 361 CCATCT 420  
DB 457 CCATCT 516  
QY 421 GGAATCGCATCGAGAGAGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 480  
DB 517 GGAATCGCATCGAGAGAGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 576  
QY 481 AAGAAGAAACGAG 540  
DB 577 AAGAAGAAACGAG 636  
QY 541 GGTCCCAAGCGGAG 600  
DB 637 GGTCCCAAGCGGAG 696  
QY 601 ACACACCGGTAGATCATGTCTGTAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 660  
DB 697 ACACACCGGTAGATCATGTCTGTAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 756  
QY 661 CCAAGGCAACT 720  
DB 757 CCAAGGCAACT 816  
QY 721 TACTGAGACGCT 780  
DB 817 TACTGAGACGCT 876  
QY 781 AGCACTTTCATACGAGAGAGTCTAGAGCCACCAATGTTTCTCGAGGCGAATCTTG 840

DB 877 AGCACTTTCATACGAGAGAGTCTAGAGCCACCAATGTTTCTCGAGGCGAATCTTG 936  
QY 841 TTAGAGCAAGGCGGCT 900  
DB 937 TTAGAGCAAGGCGGCT 996  
QY 901 GCTTGAAAGCACTTGAAGTTGGAGTGTCTCAAGAGAGAGAGAGAGAGAGAGAGAGAG 960  
DB 997 GCTTGAAAGCACTTGAAGTTGGAGTGTCTCAAGAGAGAGAGAGAGAGAGAGAGAGAG 1056  
QY 961 GAGATCATGAGAGAGAGTTCACACAGGAGATCTGTCTCTCTCTCTCTCTCTCTCTCT 1020  
DB 1057 GAGATCATGAGAGAGAGTTCACACAGGAGATCTGTCTCTCTCTCTCTCTCTCTCTCT 1116  
QY 1021 GGTGCCAAAAGATGTCTGTCTATGAGTTGTTCTTCAACAATCTCGAGCTTCACTTC 1080  
DB 1117 GGTGCCAAAAGATGTCTGTCTATGAGTTGTTCTTCAACAATCTCGAGCTTCACTTC 1176  
QY 1081 CATGGGAGAGAGCGGCTTCAATGGAATGAGACCAAGATGGAAGTTGCTTGGATCT 1140  
DB 1177 CATGGGAGAGAGCGGCTTCAATGGAATGAGACCAAGATGGAAGTTGCTTGGATCT 1236  
QY 1141 GCTAAAGACTTCTTATCTCTATGGAAGATGGAATCTTCAATCTTCACTCTCTCTATTC 1200  
DB 1237 GCTAAAGACTTCTTATCTCTATGGAAGATGGAATCTTCAATCTTCACTCTCTCTATTC 1296  
QY 1201 AAGCTTCAAAATATGATGATGATTTCAAGTTTGAAGTTGAAGTTGCTGATTTTGGCTT 1260  
DB 1297 AAGCTTCAAAATATGATGATGATTTCAAGTTTGAAGTTGAAGTTGCTGATTTTGGCTT 1356  
QY 1261 GCTAAAGTTGCTTCTATCTTCAAAACAGGATGATGATGATGATGATGATGATGATGAT 1320  
DB 1357 GCTAAAGTTGCTTCTATCTTCAAAACAGGATGATGATGATGATGATGATGATGATGAT 1416  
QY 1321 TACTGAGCTCCGAGATACGCTGCAAGCGGAGAACTCAAGAGAGTCTGAGTTTCTCA 1380  
DB 1417 TACTGAGCTCCGAGATACGCTGCAAGCGGAGAACTCAAGAGAGTCTGAGTTTCTCA 1476  
QY 1381 TTTGGGCTGTGCTTTTGGAGCTCATTACTGAGAGTGTGAGCCGTTGATGCAAAATGTC 1440  
DB 1477 TTTGGGCTGTGCTTTTGGAGCTCATTACTGAGAGTGTGAGCCGTTGATGCAAAATGTC 1536  
QY 1441 TATGTAGATACAGCTTATGTTGATCTGGGACGACCATTTGCTTACCGAGATCTGAGCAA 1500  
DB 1537 TATGTAGATACAGCTTATGTTGATCTGGGACGACCATTTGCTTACCGAGATCTGAGCAA 1596  
QY 1501 GGAAGCTTTGAGGTTTATGCTGATGCAAAAGATGATTAATGAGTATGACAGAGAGATG 1560  
DB 1597 GGAAGCTTTGAGGTTTATGCTGATGCAAAAGATGATTAATGAGTATGACAGAGAGATG 1656  
QY 1561 GCTCGATGCTGTGCTGTGCTGCGGCTTGTGCTGCTTCAATTCAGCTCGCGCGACCTGCG 1620  
DB 1657 GCTCGATGCTGTGCTGTGCTGCGGCTTGTGCTGCTTCAATTCAGCTCGCGCGACCTGCG 1716  
QY 1621 ATGAGCCAGATTTGCTGTGCTTGAAGAGAAATGATATCACTGTAGATCTTAAAGAGG 1680  
DB 1717 ATGAGCCAGATTTGCTGTGCTTGAAGAGAAATGATATCACTGTAGATCTTAAAGAGG 1776  
QY 1681 ATGAGCCAGGTTCAAAAGATGATATGAGCTCATACGAGAGAGACCCGATTATGACTCG 1740  
DB 1777 ATGAGCCAGGTTCAAAAGATGATATGAGCTCATACGAGAGAGACCCGATTATGACTCG 1836  
QY 1741 AGCCAGTACATGAAAGATGAAAGATTTTGAAGAAATGGAACCTTGAACCTGAAGATC 1800  
DB 1837 AGCCAGTACATGAAAGATGAAAGATTTTGAAGAAATGGAACCTTGAACCTGAAGATC 1896  
QY 1801 AAGCCAGAGGTTGAGTACAGTAATCCGACCAAGTGAATGAGCTTGAACCTGCTGCTTCA 1860  
DB 1897 AAGCCAGAGGTTGAGTACAGTAATCCGACCAAGTGAATGAGCTTGAACCTGCTGCTTCA 1956  
QY 1861 AGCAGCGAGGCGCAAAACCAACGCGAAATGAGATGAGGAGATTTAAGAGAAACCGGTGAG 1920  
DB 1957 AGCAGCGAGGCGCAAAACCAACGCGAAATGAGATGAGGAGATTTAAGAGAAACCGGTGAG 2016



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Db      1908 ACTATGTAGCTTCTCA---TGAAGCTCAGATTATGACACTGCACAGTACCAAGAGAGAC 1964
QY      1759 ATGAAGAAGTTTGGAAAAATGGCACTTGGAACTCAAGAGTACCAAGCGCAGGGTGAATAC 1818
Db      1965 ATGAAAAAGTTCCAGAAAAATGGCAATGGGAATCTCAGAGATGATGGTGAACAGTGAATAC 2024
QY      1819 AGTAAATCCGACCAAGTGAATGAGTGAATGAGTGAATGAGTGAATGAGTGAATGAGTGAATGAGT 1870
Db      2025 AGTGGCGCTTCAAGTGAATGAGTGAATGAGTGAATGAGTGAATGAGTGAATGAGTGAATGAGT 2084
QY      1871 -GCCAAACCAACAGCGCAATGAGATGGGAGATTAAGAAACCGTCAAGGTTATAGT 1929
Db      2085 CGCCAAACCAACAGCGCAATGAGATGGGAGATTAAGAAACCGTCAAGGTTATAGT 2141
QY      1930 GGAACCTTCT 1938
Db      2142 GGAAGTTCT 2150

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RESULT 4
US-10-425-114-9117
; Sequence 9117, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OR INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 9117
; LENGTH: 1424
; TYPE: DNA
; FEATURE: Glycine max
; ORGANISM:
; OTHER INFORMATION: Clone ID: 700833950_FLI
US-10-425-114-9117

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Query Match      33.0%; Score 642.2; DB 16; Length 1424;
Best Local Similarity 71.2%; Pred. No. 1.8e-171;
Matches 912; Conservative 0; Mismatches 348; Indels 21; Gaps 4;

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QY      673 CCTCACCCTCCACCAACCGCTTTCATGAGCAGCAGCGGCTCCG-----ACTACTCG 726
Db      9   CTTCCCCCAACCAACCGCTTTCATGAGCAGCAGCGGCTCCG-----ACTACTCG 68
QY      727 GACCGTCAAGTCTTCTCCACCGTCTCCAGGCGTTTGAAGCTTCTCCAAAAGCACT 786
Db      69 GGGGGGGAATTTCTTCTCTCTCTCTCTCTCCAGAAATTCATTGGGGTTCTCTAAAGACA 128
QY      787 TTCACTACGAGAGCTTACTAGAGCCCAATGTTTCTCCAGCGCAATTTGTTAGA 846
Db      129 TTCACTACGAGAGCTTACTAGAGCCCAATGTTTCTCCAGCGCAATTTGTTAGA 188
QY      847 CAAGGGGGGTTGGTTACGTGACCAAAAGTGTGCTTACTAGTGGAAAGAGTTGCTG 906
Db      189 CAAGGGGGGTTGGTTACGTGACCAAAAGTGTGCTTACTAGTGGAAAGAGTTGCTG 248
QY      907 AAGCACTTGAAGTTGGAGTGTGTCAGGAGAGAGGAGTTTCAAGCAAGGTTGATC 966
Db      249 AAGCACTTGAAGTTGGAGTGTGTCAGGAGAGGAGGAGGAGTTTCAAGCAAGGTTGATC 308
QY      967 ATAGAGAGAGTTACCAAGAGGATCTGTCTCTTGTGGTATGATCGCGGTGCC 1026
Db      309 ATAGAGAGAGTTACCAAGAGGATCTGTCTCTTGTGGTATGATCGCGGTGCC 368

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QY      1027 AAAAGATGCTTGTCTATGAGTTTGTCTTAACAACAATCTCGAGCTTCACTCATGAGC 1086
Db      369 CAGAGGCTCTGTTTATTAATTTGTTCCCAACAACAATGGAATTCATTGATGAGCA 428
QY      1087 GAGGAGCGGCTTCAACAATGAGATGAGCAGCAGATTTGAAGTTGCTTGGATCTGCTAAA 1146
Db      429 AAGGAGAGCTTCAACAATGAGATGAGCAGCAGATTTGAAGTTGCTTGGATCTGCTAAA 488
QY      1147 GAGCTTCTTATCTTATGAGATGAGTGAATGAGTGAATGAGTGAATGAGTGAATGAGTGAATGAGT 1206
Db      489 GAGCTGCGGTATCTTATGAGATGAGTGAATGAGTGAATGAGTGAATGAGTGAATGAGTGAATGAGT 548
QY      1207 TCAACATATGATTAATTTCAAGTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1266
Db      549 GCCAACATCTTCTGATTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 608
QY      1267 ATTGCTTCTGATTAACAACAGCATGATCAACAAGTGTGATGGGAACTTTGGTACTTG 1326
Db      609 TTTTCTTCTATGATTAACAACAGCATGATCAACAAGTGTGATGGGAACTTTGGTACTTG 668
QY      1327 GCTCCGGAATACGCTGCAAGCGGAAAGCTCAAGGAAAGTGTGATGCTTCTCATTTGGC 1386
Db      669 GCTCCGGAATACGCTTCTGATGAAATCAAGCAACAAATCAGATGTTTCTCTCATGGA 728
QY      1387 GTTGTGCTTGTGAGCTTCTTACTGAGAGTGAAGCGGCTGATGCCAACAATGCTATGTA 1446
Db      729 ATCATGCTCTTGTGATTAACAAGCGAGCGGAGTGAATTAATAATCAAACTTACATG 788
QY      1447 GATGACAGCTTAGTGAATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1506
Db      789 GAGATAGTTTGTGATGATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 848
QY      1507 TTTGAGGTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1566
Db      849 TTTGATCTTATTAATGAGCAGGCTCCAGATATGATGATCTCTCATGAGATGAGTGAAG 908
QY      1567 ATGTTGCTTGTGAGCTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1626
Db      909 ATGTTGCTTGTGAGCTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 968
QY      1627 CAGATTTGCTGCTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1686
Db      969 CAGATTTGCTGCTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1028
QY      1687 CCAAGTCAAGCAATGATTAACAGCTTCAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1746
Db      1029 CTTGAGACAGCAATGATTAACAGCTTCAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1085
QY      1747 TACAATGAGAGCATGAAGATTTAGAAATGCACTTGAATCAAGAGTACCAAGAGAGAGAGAGAGAGAG 1806
Db      1086 TACAATGAGAGCATGAAGATTTAGAAATGCACTTGAATCAAGAGTACCAAGAGAGAGAGAGAGAGAG 1145
QY      1807 ACGGCTGAGTACAGTAAATCCGACAGTGAATGAGTGAATGAGTGAATGAGTGAATGAGTGAATGAGT 1866
Db      1146 ACGGCTGAGTACAGTAAATCCGACAGTGAATGAGTGAATGAGTGAATGAGTGAATGAGTGAATGAGT 1205
QY      1867 GAGG-----GCCAAACCAACAGCGCAATGAGATGAGGAGAGAGAGAGAGAGAGAGAGAGAG 1917
Db      1206 GAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1262
QY      1918 CAGGCTTATGAGTGAAGTCTT 1938
Db      1263 CAGGCTTATGAGTGAAGTCTT 1283

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RESULT 5
US-10-437-963-59942/C
; Sequence 59942, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua

```

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1  APPLICANT: Cao, Yongwei
2  APPLICANT: Wu, Wei
3  APPLICANT: Boukharov, Andrey A.
4  APPLICANT: Barbazuk, Brad
5  APPLICANT: Li, Ping
6  TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
7  TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
8  FILE REFERENCE: 38-21 (53221)B
9  CURRENT APPLICATION NUMBER: US/10/437,963
10 CURRENT FILING DATE: 2003-05-14
11 NUMBER OF SEQ ID NOS: 204966
12 SEQ ID NO 59942
13 LENGTH: 1896
14 TYPE: DNA
15 ORGANISM: Oryza sativa
16 FEATURE:
17 OTHER INFORMATION: Clone ID: PAT_MRT4530_61518C.1
18 US-10-437-963-59942

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	Query Match	32.9%	Score 640:	DB 17:	Length 1896:
	Best Local Similarity	68.4%	Pred. No. 8.7e-171:		
	Matches 947:	Conservative 0:	Mismatches 425:	Indels 12:	Gaps 4:
QY	546	CAAAAGCCGAGAGACCTTACGCTGAGCAGAGAGACAACATGGCGGCAACAAAGCAACGC	605		
DB	1800	CAAGAGAGATGCATATGCTGGATTCATACAGAAAGTTGGCGCAAAATGCCCAACGC	1741		
QY	606	ACCGTCAGATCATGTTCGTAGCTCACTACACACACACCTAAGC---TCCATCTCCACC	662		
DB	1740	TCCGGCTGAGATGTAGTGAATGATGACCCCATCACTCCGGCAGGGTATGCAAAACCGTCC	1681		
QY	663	ACGGCAACCTCCATCCACCTCCACACCGGCTTTCATGACAGACAGCGCGCTCCGAC-	720		
DB	1680	TTCACAGCCACCATGACCCCTCCACGCTGTATGATAACACACACGGTGGGTCTGGGCTC	1621		
QY	721	-TACTCGAACCTCCAGTCTTCTCTCCACCGTCTCCAGGGCTTGTGTAGGCTTCTCCAA	779		
DB	1620	TTACTCAGGTGAGAGATCTTACCAACACATCCCTGGCGCTGGCTTGTCTCCAA	1561		
QY	780	AAGCACTTTCACATACGAGAGCTAGCTAGACCACCAATGTTTCTCCAGGCGCACTT	839		
DB	1560	GAGCACAATTACTTATGAAGACTGTGAGGCAACGATGATCTCTGATGCTAATCT	1501		
QY	840	GTTAGGACAAGCGGGGTCCGTTACGTGCAAAAGTGTGTGCTCCATGCGAAAGAGT	899		
DB	1500	CCTTGGACAAGGTGGTTTGGCTATGTCATAGAGAGTGCCTCACTGGAAAGAGAT	1441		
QY	900	TGCTGTGAAGCAGTTGAAGTTGGGAGGTCAGAGGACAGAGGAGTTTCAGGCAAGGT	959		
DB	1440	TGCTGCGAAACAATTGAAAGTTCTTAGTGGCCAGGTAAAGGTGAAATTCACAGGCGAGGT	1381		
QY	960	TGAGATCATCAGCAGAGTTTCAACAAGGCATCTGGTGTCTTGTGGTATTCATATCGC	1019		
DB	1380	TGAGTATTCAGCAGAGATCAATCAAAACATCTGCTCCATGGGTGTATTCATATTC	1321		
QY	1020	CGGTGCCAAAAGATTGCTTGTCTATAGATTGTTCTTAACAACAATCTCGAGCTTCACT	1079		
DB	1320	TGGGGGCAAGAGATTGCTTGTCTATAGATTGTCCCCAACAAACATTTGGAATTCACATT	1261		
QY	1080	CCATGGCGAGGGAGGGGCTCAATAGGAATGAGACACAGATTGAAGTTGCTCTTGATC	1139		
DB	1260	GCAACGAAAGGCGGACCAACAAAGAGGTGGCCCAAGAGCTAAAGATTGCTTGGAGAC	1201		
QY	1140	TGCTAAAGACATTTCTTATCTTCAATGAAGATTGCAATCCATAATTCATACCGTGTAT	1199		
DB	1200	TGCAAAAGGTTTACTTATCTTTCATGAAGACTGCAATCTTAAGTTCATCAATGCTGATAT	1141		
QY	1200	CAGGCTTCAAACATATGATAGATTTCAAGTTGAAGCTAAGTTGCTGATTTGGTCT	1259		
DB	1140	TAAAGGCTCAACAATCTCTTGTATTTTAAATTGATCTAAGGTTGCTGATTTGGACT	1081		
QY	1260	TGCTAATATGCTTCTGATCAAAACAGCATGATCAACAGTGTGATGGAACTTTGG	1319		

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Db      1080 TGCTAAGTTACACAGATATATAACACTCACTAGTTTCCACAAGATATAGGCACTTTGG 1021
QY      1320 GTACTTGGCTCCGGAATACCGTCGAACGGAAAGCTCACGAGAAGTCGACGTTTCTC 1379
Db      1020 ATATCTAGACCAAGAGTACCATCTTCTGGCAAGCTCACTGAGAAATCAGATGCTTCTC 961
QY      1380 ATTGGCGTTGTCGTTTGGAGCTCATTTACTGACGTCGACCCGTTGATGCCAACATGT 1439
Db      960 CTATGAGATTATCTCTTGAATTAATCACTGTCGTCGCGACGTTGATACAACTCAAC 901
QY      1440 CTATGTAGATGACAGCTTAGTTGACTCTGGGACGACCAATGCTTAAACGAGACTGAGCA 1499
Db      900 ATATATGATGATGACAGCTTGGTTACTCTGGCAAGCCCTTTACTGATGCAAGCACTTGA 841
QY      1500 AGGAGACTTTGAGGGTTTACGCTGATGCAAGATGAAATATGATGGTATGACAGAGAGAT 1559
Db      840 TGGTACTACGAGAGAGTTAGTAGATCCTCGGCTTGGCAAGSATTCAATCCAAATGAGAT 781
QY      1560 GGCTGCCATGTTGCTCTTGTGCTCGGCTTGTGTCGCCATTGACCTGCGCGAGACCTCG 1619
Db      780 GGGGAAATGATTTGCTGTGTCAGCTGATGTGACGCAATTCGCTCGTGTGCGCCACG 721
QY      1620 CATGAGCCAGATTTGTGTCGTCGCTTAGAAGGAATATGTCACGTGCAATCTTAAACGAAG 1679
Db      720 CATGAGCCAGCTTGTCCGGCTTTGGAGGTGACGTCTCTTTGGAGGATCTTAAATGAAG 661
QY      1680 GATGAGACCAAGCTCAAAAGCAATGTATACAGCTCATACGAGSAGAACCCGATTATGACTC 1739
Db      660 TGTTCGGCTGTGATCAGCGCGCTAATTTGGATGTGAC---AGCAGCTCTGACTTATGATTC 604
QY      1740 GAGCCAGTCAATGAAAGATGAAAGATTAGAAATATGCCACTTGGAACTCAAGAGTA 1799
Db      603 TGGCCAAATCAACGAGGACATGAAAGTTACAGAAAGATGCTTTT---ACCAACAATAA 547
QY      1800 CAACCCACGCGGTGAGTACAGTAAATCCGACCAAGTACTATGAGCTGTACCCGTTGCTTC 1859
Db      546 TGATACGAGCACTCATATACGCGCACCAACCAACGAGTATGGCCAGTACCTCTTGATC 487
QY      1860 AAGCAGCGAAGGGCCAAACCCACACGCGCAAAATGAGATGGGGAGATTAAAGAACCGGTCA 1919
Db      486 AAGCAGCGAAGGGCCAAACCCACAGGAATGCGAGACAGSACAAACCAAGAGAGCGGCTA 427
QY      1920 GGGT 1923
Db      426 CAGT 423

RESULT 6
US-10-425-114-2326
; Sequence 2326, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 2326
; LENGTH: 1724
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700209610_FLI
US-10-425-114-2326
Query Match      32.1%; Score 624.6; DB 16; Length 1724;

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Best Local Similarity 65.5%; Pred. No. 2e-166;  
Matches 1001; Conservative 0; Mismatches 504; Indels 24; Gaps 5;

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QY 415 GTCGTGGGAATGCCATCGGAGAGATCGCTCGCTTGTGATGTAGCTGTGTTGTCTC 474
Db 1 GTCGTGGGAGTGGCCGCTCGGCGCCCTGTGTCTGTCTGTCTCGACGCTTCACTGTCTCTC 60
QY 475 CTCGTG---AGAGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 531
Db 61 TGTGTGTCTCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
QY 532 CCTCTCTGTGTCTCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 591
Db 121 CGGCCCCCGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
QY 592 CA---AAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 639
Db 181 AATGCGCTCTGTCTCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
QY 640 CCACTTAAGGCTCATCTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 699
Db 241 GCAATATGCCAATGTCTCTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
QY 700 AGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 759
Db 301 AGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 360
QY 760 CTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 819
Db 361 GCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 420
QY 820 GCTTCTCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 879
Db 421 GGAATCTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
QY 880 TTGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 939
Db 481 CTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 540
QY 940 AGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 999
Db 541 CGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 600
QY 1000 CTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1059
Db 601 TTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 660
QY 1060 AACATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1119
Db 661 AACATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 720
QY 1120 TTGAAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1179
Db 721 TTGAAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 780
QY 1180 AAAATCATTCACCGGATATCAAGGCTTCAACATATTTGATGATTTCAAGTTGAAGCT 1239
Db 781 AAGATCATTCATCGTACATTAAGGATCATTAATTTCTTGAATTTCAAGCT 840
QY 1240 AAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1299
Db 841 AAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900
QY 1300 CGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1359
Db 901 AGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 960
QY 1360 GAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1419
Db 961 GAAAAATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1020
QY 1420 CCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1479

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Db 1021 CCAAGTTGACAGACCAACCAATATATGATGACAGCTTGTGTGCTGGCAAGCCATTA 1080
QY 1480 CTTAACCGAGATCTGAGCAGAGAGACTTTGAGGTTTATAGCTGATGCAAAAGATATAT 1539
Db 1081 CTGATGCAAGACTTGAGAGATGTGTATATATATGTCTTTATAGTATCTCGGCTGGGAAAG 1140
QY 1540 GGGTGTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1599
Db 1141 GACTTCAATCTTAATGATGTGCAAGAAATATAGCTGTGTGCAAGCTGTGATGTATAGCCAT 1200
QY 1600 TCAGCTCGGCGGAGACTTGTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1659
Db 1201 TGTGACAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1260
QY 1660 CTGTGATCTTTACAGAGAGATGAGACAGAGCTCAAGAGAGAGATATACAGCTCATAGGA 1719
Db 1261 TTGAGAGAGCTTTAATGAGAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1317
QY 1720 GGAAGACCGGATTTAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1779
Db 1318 AGCAGCTCGGATTTAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1377
QY 1780 GCACTTGAACTGAGAGATGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1839
Db 1378 GCAAT---CAACAAACATATACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1431
QY 1840 GGACTGTACCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1899
Db 1432 GGAAGATACCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1491
QY 1900 AAGATTAAGAGAACCGGTGAGGTTATAG 1928
Db 1492 GCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1520

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RESULT 7  
US-10-425-115-57011  
; Sequence 57011, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yinhua  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53222)B  
; CURRENT APPLICATION NUMBER: US/10/425,115  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326  
; SEQ ID NO 57011  
; LENGTH: 2886  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: MRT4577\_151984C.1  
US-10-425-115-57011

Query Match 32.0%; Score 621.2; DB 18; Length 2886;  
Best Local Similarity 67.1%; Pred. No. 2.4e-165;  
Matches 948; Conservative 0; Mismatches 443; Indels 21; Gaps 4;

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QY 529 CCACTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 588
Db 1172 CGGCGCCCGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1231
QY 589 CAACA---AAAGCAACACCGTCAATCATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 636
Db 1232 CAATAAGGCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1291
QY 637 CCAGCACTTAAGGCTCATTTTCACACAGGAGAACTTCTTCACTTCCACACCGCTTTC 696
Db 1292 CCAGGAGTTTCAATGATCTTCAAAACAGGCGCGCCACCAACAGCGATGTCTAAT 1351

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QY 697 ATGAGCAGCAGCGGCGCTCCGACTCTGAGACCGTCCAGTTCTTCTCCACCGCTTCCA 756  
 DB 1352 AGTGTGTGTGATCTGTTCTTAATTACTCTGTGTGCGAGATCTCACTCCACCATCCCTT 1411  
 QY 757 GGGCTGTGTAGAGCTTCTCCAAAGCACTTCACTACGAGGAGTACGTAGAGCCACC 816  
 DB 1412 GGTCTGTCTTGTGCTCTCTGAAAGACATCTTCACTACGAGGAGTGTGAGGCTTACT 1471  
 QY 817 AATGCTTCTCCGAGCGAACTTGTAGACACAGCGCGTTCGCTTCACTGACAAAGT 876  
 DB 1472 GATGTATCTCTGATGCTAATCTCTTGGACCAAGTGTGTTTGTCTATGTTTCAAGAGA 1531  
 QY 877 GTGTGCTGTGAGGAAAGAGTGTCTGTAGAGCACTTGAAGTTGGAGTGTCAAGGGA 936  
 DB 1532 TTGCTGCTTAATGCAAGAGATGTGTAAATAATGAACTGGAGAGTGGCAGAGGA 1591  
 QY 937 GAGAGGAGTTCAGCAGAGGTTGAGATCATCAGCAGAGTTCACACAGCAATCTGTG 996  
 DB 1592 GAGGTGAGTTCAGCAGGCTGAGGTTGAGATTCACGCGAGTACATCAACAAACCTTGTG 1651  
 QY 997 TCTCTGTGTGTTATTCATCTGCGCGTGCACAAAGATGTGTCTATGAGTTTGTCT 1056  
 DB 1652 TCTTGTGTGCTATTCATCTTCTGAGCAGAGGCTGCTGTCTATGAGTTTGTCTCC 1711  
 QY 1057 AACACATCTGAGCTTCACCTCCATGCGAGAGGAGCGCTTCAATGATGAGACAC 1116  
 DB 1712 AATTAACATTCGAAATTCACCTTACATGCGAAAGGTGACCAACATGAGTGGCTGTCT 1771  
 QY 1117 AGATTGAAGTTGCTCTGTGATCTGCTAAAGACCTTCTATCTTCAATGAAGTTGCAT 1176  
 DB 1772 AGATTGAAGTTGCTGTGCTGTGCTGCGAAGGTTTGTGCTTATCTTCAATGAAGTTGCAT 1831  
 QY 1177 CCTAAATCTTACCGTGTATCAAGCTTCAACATATGATGATTCAGTTTGA 1236  
 DB 1832 CCMAAGATCATCTGATGACATTAAGGACATTAATCTTCTGACCTTCAATTTGA 1891  
 QY 1237 GCTAAGTTGCTGATTTGCTGTGTGATGATTTGCTTGTATCAAAACGCAATGATCA 1296  
 DB 1892 GCTAAGTTGCTGATTTGCTGTGTGATGATTTGCTTGTATCAAAACGCAATGATCA 1951  
 QY 1297 ACAAGTGTATGGAACCTTGTGTGCTTGTGCTGCGAATGACCTGCAAGCGGAAGCTC 1356  
 DB 1952 ACAAGTGTATGGAACCTTGTGTGCTTGTGCTGCGAATGACCTTGTGCAAGCTCA 2011  
 QY 1357 AGGAGAACTGACGTTTCTCATTTTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 1416  
 DB 2012 ACAGAAAAATCCGATGTATTTCTTGTGAGTCACTGCTTCTGAGCTTATTACTGGCGG 2071  
 QY 1417 CGACCGTGTATGCAACAATGTCTATGATGACAGCTTGTGATGATGATGATGATGATGAT 1476  
 DB 2072 CGACCGTGTATGCAACAATGTCTATGATGACAGCTTGTGATGATGATGATGATGATGAT 2131  
 QY 1477 TTGCTTAAACGAGCATCTGAGCAAGAGACCTTGAAGGTTTGTGATGATGATGATGATGAT 1536  
 DB 2132 TTACTGATGCGAGCATCTGAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 2191  
 QY 1537 AATGGTATGACAGAGAGAGATGCTGCGATGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 1596  
 DB 2192 AAGGCTTCAATCTTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2251  
 QY 1597 CATTCAGCTGCGCGAGACCTGCAATGAGCCAGATTTGCGCGTGTGAGAAAGAAATGTA 1656  
 DB 2252 CATTCAGCTGCG 2311  
 QY 1657 TCACCTGTCAGTCTTAAAGAGGATGAGACAGGCTCAAGAGCAATGTAACAGCTCATAC 1716  
 DB 2312 TCTTTGAGGACCTTAAATGAAGTGTGTGCGCTGCGCATAGCGCTTCTTTGGCTCATAC 2371  
 QY 1717 GAGAGAGCAGCAGTATGATCTGAGCGAGTACATGAAGAATGAAGAAGTTTGAAGAA 1776  
 DB 2372 ---AGCAGCTCCGATTCGATTCGAGTTCGCGCAGTACAAAGAGCATGAAGAGTTCAAGAG 2428

QY 1777 ATGCACTTGGAACTCAAGAGTACACAGCGGAGTGTAGTACAGTAATCCGACCATGTAC 1836  
 DB 2429 ATGCACTT-----CAACAACTATATACAGCAGCCATATACAGCGCGCAACAGTGA 2482  
 QY 1837 TATGACTGTACCCGTGTGTGTTCAAGCAGCGAGCGCCAAACACAGCGGAATGAGATG 1896  
 DB 2483 TATGACAGATATCCGTCTGATCAAGCAGGAGCGCCACCGAGCAGCAAGATGTAGTGC 2542  
 QY 1897 GGGAGATTAAGAAACCGGTCAAGTTATG 1928  
 DB 2543 GGTGCAATGAAGAAAGGTGCTACAGTGTG 2574

RESULT 8  
 US-10-425-114-33030  
 ; Sequence 33030, Application US/10425114  
 ; Publication No. US20040034888A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Liu, Jindong  
 ; APPLICANT: Zhou, Yihua  
 ; APPLICANT: Kovalic, David K.  
 ; APPLICANT: Screen, Steven B  
 ; APPLICANT: Tabaska, Jack E  
 ; APPLICANT: Cao, Yongwei  
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
 ; FILE REFERENCE: 38-21(5313)B  
 ; CURRENT APPLICATION NUMBER: US/10/425,114  
 ; NUMBER OF SEQ ID NOS: 2003-04-28  
 ; SEQ ID NO 33030  
 ; LENGTH: 2880  
 ; TYPE: DNA  
 ; ORGANISM: Zea mays  
 ; FEATURE:  
 ; OTHER INFORMATION: Clone ID: UC-ZMPLMO17055B11\_F11  
 US-10-425-114-33030

Query Match 31.9%; Score 619.6; DB 16; Length 2880;  
 Best Local Similarity 66.7%; Pred. No. 6,8e-165;  
 Matches 918; Conservative 0; Mismatches 449; Indels 9; Gaps 2;

QY 553 GGAGGACCTTACGATGAGCAGCAGCAACATGCGCGCAACAAACGACACACACCGTCA 612  
 DB 1258 GGTGGAACGTACCAAGATGTGCGAGCAAAATGCGCTTCTGCTCCACCCCTGAACATGTG 1317  
 QY 613 GATCATGTCTGATGCTGCTATCACCACTCACTTAAGCTTCACTTCCACACGCAACCT 672  
 DB 1318 GTCAAGATGACACCTTGTGCTTCCGCGCATATGCGCAATGTCTTCCACACGCGCAGCG 1377  
 QY 673 CCTCCACCTCCACACCGCGCTTCTATGAGCAGCAGCGCGCGCTCCGACATCTCCGACCGT 732  
 DB 1378 CCGCCACCAACGACGATGTCTAATATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1437  
 QY 733 CGAGTTCTTCTCCACCGCTTCTCCAGCGCTTGTAGGCTTCTCCAAAGCACTTTCACA 792  
 DB 1438 GAGATCTTACCTCCACCATCTCCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1497  
 QY 793 TACGAGGAGTATGATGAGGACCAACCATGTTTCTCCAGCGCACTTGTGAACAAGGC 852  
 DB 1498 TACGAGGAGTATGAGGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1557  
 QY 853 GGGTTCGGTTACGTCACAAAGT 912  
 DB 1558 GGTTCGGTTACGTCACAAAGT 1617  
 QY 913 TTGAAAGTTGAGTGTGTCAAGGAGAGAGAGAGTTCAGCAGAGTGTGATCATTCAGC 972  
 DB 1618 TTGAAAGTTGAGTGTGTCAAGGAGAGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1677  
 QY 973 AGAGTTCAACAGAGCATCTGTGTGTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1032  
 DB 1678 CGAGTATCATCAACAAACCTTGT 1737



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QY 1033 TTGCTTGTCTATGAGTTTGTCTTAAACAACAATCTCGAGCTTACCTCCATGCGAGGA 1092
Db 1738 CTGCTTGTCTATGAGTTTGTCTTAAACAACAATCTCGAGCTTACCTCCATGCGAGGA 1797
QY 1093 CGGCTTCAATGGAATGAGACACGAGATTGCTCTTGGATCTCTTAAAGACTT 1152
Db 1798 CGACCAACAATGAGAGTGGCTCTAGATTAAAGATCAATTGGGCTCCCAAGGTTTA 1857
QY 1153 TCTTATCTTCAATGGAATGGAATCTTAAATCATTCACCGGATTCAGAGGCTTCAAC 1212
Db 1858 GCTTATCTTCAATGGAATGGAATCTTAAATCATTCACCGGATTCAGAGGCTTCAAC 1917
QY 1213 ATATTGATGATTTTCAAGTTTGAAGTTGCTGATTTTGTCTTAAAGATTGCT 1272
Db 1918 ATTCTTCTTGAATCTTCAATTTGAAGTTGCTGATTTTGTCTTAAAGATTGCT 1977
QY 1273 TCTGATACAAACGCGATGTATCAACACGTTGATGGAACCTTTGGGTTCTTGGCTCG 1332
Db 1978 ACTGATACAAACGCGATGTATCAACACGTTGATGGAACCTTTGGGTTCTTGGCTCG 2037
QY 1333 GAATAGCTTCAAGCGGAAGCTCAAGGAATGAGCTTCTTCAATTTGGGCTTGG 1392
Db 2038 GAGTATGCAATCTTCTGCAAGCTTACAGAAAAATCGATGTATTTCTTGGAGTCATG 2097
QY 1393 CTTTGGAGCTCATTACTGAGAGCTGACCCGTTGATGCGCAACAATGCTATGTAGATGAC 1452
Db 2098 CTCTTGAATTTTACTGAGCGGCGGACGACGAGTTGACCAACCAACATATATGAGTAC 2157
QY 1453 AGCTTATGACTGAGGACGACCATTTGCTTAACTGAGACCTTGAAGCAAGACCTTGGAG 1512
Db 2158 AGCTTATGACTGAGGACGACCATTTGCTTAACTGAGACCTTGAAGCAAGACCTTGGAG 2217
QY 1513 GCTTATGCTATGCAAAAGATGAATATGAGGATGACAGAGAGGAGTGGCTCGATGCTT 1572
Db 2218 GCTTATGCTATGCTATGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2277
QY 1573 GCTTATGCTATGCTATGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1632
Db 2278 GCTTATGCTATGCTATGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2337
QY 1633 GTGCTGCTGTTAAGAGGAATGATATCACTGTCACTTAAAGAGGATGACGAGCT 1692
Db 2338 GTTGGGCTTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2397
QY 1693 CAATGCAATGTATACAGTCTACGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1752
Db 2398 CATAGCGCTTCTTGGGCTATAC--AGAGCTTCCGATTAAGATTCTGAGGAGGAGG 2454
QY 1753 GAAGCAATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1812
Db 2455 GAGAGCAATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2508
QY 1813 GAGTACAGTAAATCCGACCAATGATGAGTATGAGTATGAGTATGAGTATGAGTATG 1872
Db 2509 CAATACAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2568
QY 1873 CAATACAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1928
Db 2569 CACCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2624

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RESULT 9
US-10-425-114-33031
; Sequence 33031, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei

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; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 33031
; LENGTH: 2881
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLMO17055B12_FU1
US-10-425-114-33031

Query Match      31.9%; Score 619.6; DB 16; Length 2881;
Best Local Similarity 66.7%; Pred. No. 6,8e-165;
Matches 918; Conservative 0; Mismatches 449; Indels 9; Gaps 2;

QY 553 GGAGGACCTTACGGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 612
Db 1259 GGTGGAAGGATACAGAGGTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1318
QY 613 GATCATGTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 672
Db 1319 GTCAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1378
QY 673 CCTGCACTTCCACCGGCTTCAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 732
Db 1379 CCGCCACACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1438
QY 733 CCAATCTTCCACCGGCTTCAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 792
Db 1439 GAGATCTTACCTTCCACCGGCTTCAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1498
QY 793 TACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 852
Db 1499 TACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1558
QY 853 GGGTTCGTTTACGTCAGCAAAAGTGTGTGCTTATGAGGAGGAGGAGGAGGAGGAGGAGGAGG 912
Db 1559 GGGTTCGTTTACGTCAGCAAAAGTGTGTGCTTATGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1618
QY 913 TTGAAATTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 972
Db 1619 TTGAAATTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1678
QY 973 AGAGTTACCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1032
Db 1679 CGAGTACATCAACAAACCTTGTGTGCTTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1738
QY 1033 TTGCTTGTCTATGAGTTTGTCTTAAACAACAATCTCGAGCTTACCTCCATGCGAGGA 1092
Db 1739 CTGCTTGTCTATGAGTTTGTCTTAAACAACAATCTCGAGCTTACCTCCATGCGAGGA 1798
QY 1093 CGGCTTCAATGGAATGAGACACGAGATTGCTCTTGGATCTCTTAAAGACTT 1152
Db 1799 CGACCAACAATGAGAGTGGCTCTAGATTAAAGATCAATTGGGCTCCCAAGGTTTA 1858
QY 1153 TCTTATCTTCAATGGAATGGAATCTTAAATCATTCACCGGATTCAGAGGCTTCAAC 1212
Db 1859 GCTTATCTTCAATGGAATGGAATCTTAAATCATTCACCGGATTCAGAGGCTTCAAC 1918
QY 1213 ATATTGATGATTTTCAAGTTTGAAGTTGCTGATTTTGTCTTAAAGATTGCT 1272
Db 1918 ATTCTTCTTGAATCTTCAATTTGAAGTTGCTGATTTTGTCTTAAAGATTGCT 1977
QY 1273 TCTGATACAAACGCGATGTATCAACACGTTGATGGAACCTTTGGGTTCTTGGCTCG 1332
Db 1978 ACTGATACAAACGCGATGTATCAACACGTTGATGGAACCTTTGGGTTCTTGGCTCG 2037
QY 1333 GAATAGCTTCAAGCGGAAGCTCAAGGAATGAGCTTCTTCAATTTGGGCTTGG 1392
Db 2038 GAGTATGCAATCTTCTGCAAGCTTACAGAAAAATCGATGTATTTCTTGGAGTCATG 2097

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QY 1393 CTTTGAAGCTCATTACTGACGTCGACCCGTTGATGCCAACAATGCTATGTAGATGAC 1452  
|||  
Db 2099 CTTCTTGAAGCTTATTACTGGGCGGCGACCAAGTTGACCAACCAACATATATGATGAC 2158  
QY 1453 AGCTTATTGATCTGGGACGACCACTTGTCTTAACTGAGATCTGACGAAGAATTGAG 1512  
|||  
Db 2159 AGCTTATTGATCTGGGACGACCACTTGTCTTAACTGAGATCTGAGATGATGATGAT 2218  
QY 1513 GATTAGCTGATGACGAAGAATGATGATGATGATGATGATGATGATGATGATGATGAT 1572  
|||  
Db 2219 GCTTATGATGATCTCGGCTGGGAAAGACTTCAATCTTATGATGATGATGATGATGAT 2278  
QY 1573 GCTTGTGCTGCGGCTTGTGTTTGGCATTGAGCTGCGGACGACCTGCGATGAGCAGATT 1632  
|||  
Db 2279 GCTTGTGCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2338  
QY 1633 GTGCTGTGCTTAAAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1692  
|||  
Db 2339 GTTGGGCTTTGAGAGGCAATGTGTCTTTGAGAGGACCTTATGATGATGATGATGATGAT 2398  
QY 1693 CAAGCAATGATATACAGCTCATACGAGAAAGACCGATTATGATCTGAGCCAGTCAAT 1752  
|||  
Db 2399 CATAGCGGCTTCTTTGGGTCTATC---AGCAGCTCGATTTAGATTTCTGCGCAGTACAC 2455  
QY 1753 GAAGACATGAAAGATTTAGAGAAATGAGCACTTGAACTCAAGATGACAAAGCAGGCT 1812  
|||  
Db 2456 GAGGACATGAAAGATTTAGAGAAATGAGCACTTGAACTCAAGATGACAAAGCAGGCT 2509  
QY 1813 GAGTACATGATCCGACCAAGTACTATGACTGATCCGCTGTTCAAGCAGCAGGCT 1872  
|||  
Db 2510 CATATACAGCGGCGCAACCACTGATATGACAGATACCGCTGATCAACAGCAGGCT 2569  
QY 1873 CAACCAACGCGCAAAATGAGATGAGGAAAGATTTAGAGAAACCGCTGAGGTTATG 1928  
|||  
Db 2570 CACCAAGCAGAGAGATGAGTGGGTGCAATGAAAGATGCTACAGTGTGG 2625

RESULT 10  
US-10-437-963-6708/c  
; Sequence 6708, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO: 6708  
; LENGTH: 2187  
; TYPE: DNA  
; ORGANISM: *Oryza sativa*  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_13372C.1  
US-10-437-963-6708

Query Match 29.1%; Score 566.6; DB 17; Length 2187;  
Best Local Similarity 66.7%; Pred. No. 6,9e-150;  
Matches 847; Conservative 0; Mismatches 404; Indels 18; Gaps 2;

QY 523 CCTGCGCACTCTCTCTGTTCCAAAGCCGAGGACCTTACGATGACAGCAGCAANA 582  
|||  
Db 1595 CCGCGCGCGCGCGCGCGCGCGCTTCAAGGGGATCACTATGGTGGGTGTACCAAAAT 1536

QY 583 TGGCGCAACAAACGACACCAACCGTCAATGATGATGATGATGATGATGATGATGATGAT 642  
|||  
Db 1535 TGGCAGCAAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1476  
QY 643 CTTAAGCTTCATCTCCACACGCGCAACCTCTCCACCTCCACACCGCGCTTATGAGC 702  
|||  
Db 1475 CTTCCCTCC-----ACCACTCTCTCCACCTTAAATGATGATGATGATGATGATGAT 1431  
QY 703 AGCAGCGCGCGCTCCGACTACTCGGACCGTCCAGTTCTTCTCCACCGTCTCCAGGCTT 762  
|||  
Db 1430 GATTCTGCTCAAAATTAATCTCGGTGGGACCAACCCCACTTAAGTGTACCTGAGTCT 1371  
QY 763 GTGTAGGCTTCTCAAAACCACTTCACTACGAGGAGCTAGTATGAGCACAATGAT 822  
|||  
Db 1370 GATTTGGGTTTTCMAAGTGTACTTTTCACTTATGAGGACCTTGTAGGCGGACCGATGGA 1311  
QY 823 TTTCTCGAGCGCACTTTGTTAGACAAAGCGGTTGCGTTACGTCACAAAGTGTGTTG 882  
|||  
Db 1310 TTTCTCGATGCTATCTGCTCGGACAGGCGGTTTGGTATGTTTCAAAAGAGTTCTG 1251  
QY 883 CTTAGTGGGAAAGATGCTGTGAGCACTTGAAGTTGAAGTTGGAGTGTGAGGAGAG 942  
|||  
Db 1250 CCGAATGGACAGAGGTTGCTGTGAAGCAATTAAGATGAGATGGAGTGGGACGAGACGT 1191  
QY 943 GAGTTTCAGGACAGGTTGAGATCATCAGAGATTCACACAGGACATCTGTGTCTCT 1002  
|||  
Db 1190 GAATTTCAAGCGGAGGTTGAGATATCAAGCGGTTACATCAAGATCTTGTATCACTTG 1131  
QY 1003 GTTGTATTGATCGCGCGGTGCAAAAGATTTGCTATGATGATTTGTTCTTAAACAC 1062  
|||  
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QY 1888 ATGAGATGAG 1943  
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Publication No. US20020199218A1  
GENERAL INFORMATION:  
APPLICANT: GORING, Daphne R. et al.  
TITLE OF INVENTION: PROLINE-RICH EXTENSIN-LIKE RECEPTOR KINASES  
FILE REFERENCE: P 25,762-A USA  
CURRENT APPLICATION NUMBER: US/10/086,464  
CURRENT FILING DATE: 2002-02-28  
PRIORITY APPLICATION NUMBER: US 10/069,304  
PRIORITY FILING DATE: 2002-02-19  
PRIORITY APPLICATION NUMBER: PCT/CA00/00966  
PRIORITY FILING DATE: 2000-08-18  
PRIORITY APPLICATION NUMBER: US 60/149,466  
PRIORITY FILING DATE: 1999-08-19  
PRIORITY APPLICATION NUMBER: US 60/159,122  
PRIORITY FILING DATE: 1999-10-13  
NUMBER OF SEQ ID NOS: 27  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 10  
LENGTH: 1902  
TYPE: DNA  
ORGANISM: Arabidopsis thaliana  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)..(1902)  
US-10-086-464-10

Query Match 26.6%; Score 516.2; DB 13; Length 1902;  
Best Local Similarity 67.1%; Pred. No. 1.4e-135;

Matches 747; Conservative 0; Mismatches 363; Indels 3; Gaps 1;

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; APPLICANT: Kovalic, David K.  
 ; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH  
 ; FILE REFERENCE: 38-21(53377)B  
 ; CURRENT APPLICATION NUMBER: US/10/739,930  
 ; CURRENT FILING DATE: 2003-12-18  
 ; NUMBER OF SEQ ID NOS: 11088  
 ; SEQ ID NO 726  
 ; LENGTH: 2185  
 ; TYPE: DNA  
 ; ORGANISM: Arabidopsis thaliana  
 ; FEATURE:  
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 US-10-739-930-726

Query Match 26.6%; Score 516.2; DB 18; Length 2185;  
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QY	970	AGCAGAGTTCACCAAGCATCTGCTCTCTGTTGTTATGATCGCCGCTGCCAA	1029
DB	1111	AGCCGTGTCATCATCGGTATCTGTTTCTTGTGTTGATGATGATGATGATGATGATG	1170
QY	1030	AGATTGCTGTCTATGAGTTTGTCTTCAACAACTCGAGCTTCACTCGATGGCGAG	1089
DB	1171	AGGATGTTGTTATGAGTTTGTCTTCAACAACTTGAATATCATCTTCATGGGAAA	1230
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DB	1291	CTCGCTTACCTTCAAGAGACTGCGATCTCGATCATTCACCGGACATCAAGTCTGCA	1350
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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

CM nucleic - nucleic search, using sw model

Run on: November 13, 2004, 07:54:05 ; Search time 4165 Seconds  
(without alignments)  
17008.125 Million cell updates/sec

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Scoring table: IDENTITY NUC  
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Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_hic:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_gss1:\*  
9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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2	594.6	30.6	723	CD839231	CD839231 RPO2.1141
3	572.8	29.5	853	BX834233	BX834233 BX834233
4	496	25.5	1036	BX837083	BX837083 BX837083
5	442.2	22.7	759	BM408099	BM408099 EST582426
6	438.2	22.5	799	CN010757	CN010757 WHE875_G
7	429.6	22.1	757	BG596561	BG596561 EST495239
8	419.2	21.6	731	CB655196	CB655196 OSJNC08R
9	417.6	21.5	2734	CNS0A4OX	BX816903 Arabidops
10	413.2	21.3	692	BG441204	BG441204 GA_Ba001
11	411.6	21.2	584	AV534493	AV534493 AV534493
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14	405.6	20.9	789	CF436655	CF436655 EST672000
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## ALIGNMENTS

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DEFINITION  
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Arabidopsis thaliana full-length cDNA complete sequence from clone  
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ACCESSION  
BX823746.1 GI:42462388  
VERSION  
HTC; GSUT CDNA.  
KEYWORDS  
Arabidopsis thaliana (thale cress)  
ORGANISM  
Arabidopsis thaliana

REFERENCE  
Aurell, V., Aury, J.-M., Jallion, O., Wincker, P., Clepet, C.,  
Menard, M., Craud, C., Quetier, F., Scarpelli, C., Schacher, V.,  
Temple, G., Caboche, M., Weissenbach, J., and Salanoubat, M.,  
Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences:  
A Combined Approach to Evaluate and Improve Arabidopsis Genome  
Annotation  
Unpublished  
2 (bases 1 to 2106)

JOURNAL  
REFERENCE  
Genoscope.  
Direct Submission  
Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage :  
BP 191 91006 EVRY cedex - FRANCE (E-mail : sequef@genoscope.cns.fr  
- Web : www.genoscope.cns.fr)

## COMMENT

The sequences are based on single pass reads.  
Life Technologies (a division of Invitrogen) members carried out  
full-length libraries construction : Temple G.  
Genoscope members carried out sequencing and annotation : Castelli  
V., Aury J.-M., Jallion O., Wincker P., Menard M., Craud C.,  
Schacher V., Weissenbach J., Salanoubat M.  
URGV INRA : Clepet C., Caboche M.  
Annotation is based on the June 2003 version of the Arabidopsis  
genome released by MIPS (Munich Information center for Protein  
Sequences) . 5 prime and 3 prime are assembled with Phrap.  
http://www.genoscope.cns.fr/externe/sequences/Banque\_Projet\_EF/Full  
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## FEATURES

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## ORIGIN

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Matches 1601; Conservative 0; Mismatches 299; Indels 32; Gaps 5;

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DB |||||
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DB |||||
QY 91 CTCTCCACACACACACACACACACACACACACACACACACACACACACACACAC 141
DB |||||
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DB |||||
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DB |||||
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DB |||||
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QY 1123 TTACTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1182
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QY 1093 CGGCTTACATGAAATGAGACCAAGATGAAATGCTCTCTCTCTCTCTCTCTCTCTCT 1152
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DB |||||
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DB |||||
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DB |||||
QY 1873 CAAACCAACGCAAGATGAGATGAGGAAATGAAAGATGAGGATGAGGATGAGGAT 1932
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RESULT 2  
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LOCUS CD839231 723 bp mRNA linear EST 10-JUL-2003  
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SEQUENCE  
ACCESSION CD839231  
VERSION CD839231.1 GI:32521171  
KEYWORDS EST.  
SOURCE Brassica napus (rape)  
ORGANISM Brassica napus  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.  
1 (bases 1 to 723)  
REFERENCE Genoplatte, a major partnership french program in plant genomics  
AUTHORS Genoplatte, unpublished (2003)  
JOURNAL Contact: Genoplatte  
COMMENT Genoplatte  
93, rue Henri Rochefort 91025 EVRY CEDEX France  
Tel: 33 1 69 47 54 00  
Fax: 33 1 69 47 54 10  
This sequence has been generated in the framework of the french  
plant genomics programme 'genoplatte' (<http://www.genoplatte.com>  
and <http://genoplatte-info.intobio.gen.fr>).  
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Matches 597; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
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Query 1404 CATTACTGAGCGTGCACCCGTTGATGCCAACAATGCTATGATGACACTTAAGTTGA 1463  
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Query 1464 CTGGGACGACCATTTGCTTAAACGAGCATCTGAGCAAGAGACTTTGAGGTTTAACTGA 1523  
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Db 241 GGCTTGTTGTCAGCATTCAGCTCGCGGAGACTCGCATGAGCGAGANTGTCGTGGCTT 300  
Query 1644 AGAAGAAATGATCTACTGTCAGATCTTAAAGAAAGGATGAGACAGGTCAAAGCAATGT 1703  
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Db 421 GAAGTTAGAAAAATGGCTTGGAACTCAAGAGTACAAGCCACGGGTAGTACATTA 480  
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LOCUS BX834233 853 bp mRNA linear EST 11-FEB-2004  
DEFINITION BX834233 Arabidopsis thaliana Adult vegetative tissue Col-0  
SEQUENCE  
ACCESSION BX834233  
VERSION BX834233.1 GI:42517711  
KEYWORDS EST.  
SOURCE Arabidopsis thaliana (thale cress)  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
1 (bases 1 to 853)  
REFERENCE Castellani V., Aury J.M., Jallion O., Wincker P., Clepet C.,  
Menard M., Cruaud C., Querrier F., Scarpelli C., Schachter V.,  
Temple G., Caboche M., Weissenbach J. and Salanoubat M.  
Whole Genome Sequence Comparisons and 'Full-Length cDNA Sequences:  
A Combined Approach to Evaluate and Improve Arabidopsis Genome  
Annotation  
Unpublished (2004)  
JOURNAL Contact: Genoscope  
COMMENT Genoscope - Centre National de Sequencage  
BP 191 91006 EVRY cedex - France  
Email: [segreg@genoscope.cns.fr](mailto:segreg@genoscope.cns.fr), Web: [www.genoscope.cns.fr](http://www.genoscope.cns.fr)  
The sequences are based on single pass reads.  
Life Technologies (a division of Invitrogen) members carried out  
full-length libraries construction; Temple G.  
Genoscope members carried out sequencing and annotation; Castellani  
V., Aury J.M., Jallion O., Wincker P., Menard M., Cruaud C.,  
Schachter V., Weissenbach J., Salanoubat M.  
URGV INRA: Clepet C., Caboche M.  
Annotation is based on the June 2003 version of the Arabidopsis  
genome released by MIPS (Munich Information center for Protein  
Sequences).  
[http://www.genoscope.cns.fr/externe/sequences/Banque\\_Projet\\_EF/EST](http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/EST)  
<http://www.genoscope.cns.fr/cgi-bin/gdb/gdb?source=Arabidopsis>.  
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Query 1313 CTTTGGGTAATTTGGCTCGGAATATGCTGCAAGTGAAGAGTCAAGAAAGTCTGACG 728  
Db 787 CTTTGGGTAATTTGGCTCGGAATATGCTGCAAGTGAAGAGTCAAGAAAGTCTGACG 728  
Query 1373 TTTTTCATTTGGCGTTTGCTTTTGAAGCTATTACTGACGTGACCCGTTGATGCCA 1432

Db	Accession	Version	Keywords	Organism	Reference Authors	Title	Journal Comment
Db	727	CTTTTCATTGTTGGCGCTTGTA	CTTTGGA	ACTTATTA	CTGAGAGGCGCCCTGTTGATGCGA	668	
Qy	1433	ACAAATCTTATGTAGATGACAGCTTA	AGTTGACTGGGCA	GAGACCATTTGCTTAA	ACCGAGCAT	1492	
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Qy	1493	CTGAGCAAGGAGCTTTGAGGGTTTG	AGCTGATGCAAA	AGATGAATTA	TGGGTATGACAGAG	1552	
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DEFINITION	XB837083						
ACCESSION	XB837083						
VERSION	XB837083						
KEYWORDS	XB837083.1						
SOURCE	EST.						
ORGANISM	Arabidopsis thaliana (thale cress)						
REFERENCE	Arabidopsis thaliana						
AUTHORS	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosoids; eurosids II; Brassicales; Brassicaceae; Arabidopsis. 1 (bases 1 to 1036)						
TITLE	Castelli V., Aury J.M., Jailion O., Winkler P., Clepet C., Menard M., Cruaud C., Queiser F., Scarpelli C., Schachter V., Temple G., Caboche M., Weissenbach J. and Salanoubat M. Whole genome Sequence Comparisons and "Full-Length" cDNA Sequences A Combined Approach to Evaluate and Improve Arabidopsis Genome Annotation						
JOURNAL	Unpublished (2004)						
COMMENT	Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Email: secref@genoscope.cns.fr, Web : www.genoscope.cns.fr The sequences are based on single pass reads. Life Technologies (a division of Invitrogen) members carried out Full-length libraries construction : Temple G. Genoscope members carried out sequencing and annotation : Castelli V., Aury J.M., Jailion O., Winkler P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M. URGV INRA : Clepet C., Caboche M. Annotation is based on the June 2003 version of the Arabidopsis Genome released by MIPS (Munich Information center for Protein						

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SEQUENCES) .
http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/EST
http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis.
FEATURES
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Db	316	CTCTGAGATCT	375	
Qy	391	TCGACGCTTATCAACAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	450	
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Qy	451	GTGATAGTACTTGTATTTGTCTCTCTGTAAAGAAAGAAAGAAAGAAAGAAAG	504	
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Qy 922 GGGAGGCTCAGGAGAGAGAGTTTGCAGAGAGTTGATCATCAGCAGAGTTTGC 981

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LOCUS EST582426 potato roots Solanum tuberosum cDNA clone cPRO33021 5'

DEFINITION end, mRNA sequence.

ACCESSION BM408099

VERSION BM408099.1 GI:18259729

KEYWORDS EST.

SOURCE Solanum tuberosum (potato)

ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanales; Solanales; Solanales.

REFERENCE van der Hoeven, R., Sun, H., Karamehara, S.A., Tsai, J., Van Aken, S., Utebbeck, T., Chiemung, A., Bougri, O., Buell, C.R., Rinning, C., Tanksley, S. and Baker, B.

AUTHORS Generation of ESTs from potato roots

TITLE Unpublished (2001)

JOURNAL The Institute for Genomic Research

COMMENT Contact: Robin Buell  
9712 Medical Center Dr, Rockville, MD 20850, USA  
Email: potatocenter@igrr.org  
This clone can be obtained from the University of Arizona Genomics Institute. Orders can be made through URL:  
http://genome.arizona.edu/orders/  
Seq primer: T3.

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ORIGIN

Query Match 22.7%; Score 442.2; DB 4; Length 759;  
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Qy 993 GAGTCTCTTGTGTTATTCATGATGCGCGGTGCCAAAGATTGTTCTATGAGTTGT 1052

Db 61 TGTGTCTCTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120

Qy 1053 TCTTACACAAATTCGAGCTTACCTCCATGCGAGGAGCGCTTACATGAAATGAG 1112

Db 121 TCCAAACAAATCTTGGATTTTATTTACACGAAAGGAGGAGCTCTTGGATGAGCC 180

Qy 1113 CACGATTTGAAGATGCTTGTGATCTGATCAAGAGCTTTCTTATCTTCAAGAGATTG 1172

Db 181 AATACGCTAAGATGCTTGTGATGCTTGTGATCAAGAGCTTTCTTATCTTCAAGAGATTG 240

Qy 1173 CAATCTTAAATTCATTCACCGGATATCAAGGCTTCAACATATGATGATTTCAAGT 1232

Db 241 CCAACGAAATTCATTCACCGGATATCAAGGCTTCAACATATGATGATTTCAAGT 300

Qy 1233 TGAAGCTAAGTTGCTGATTTTGTGCTTGTGATGATGATGATGATGATGATGATGAT 1292

Db 301 TGAGGCTAAGTTGCTGATTTTGTGATGATGATGATGATGATGATGATGATGATGATGAT 360

Qy 1293 ATCAACAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1352

Db 361 CTCACAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420

Qy 1353 GCTCAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1412

Db 421 GCTTACAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480

Qy 1413 AGTGACCCGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1472

Db 481 AGTGACCCGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540

Qy 1473 ACCATGCTTACAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1532

Db 541 TCCATTTCTACAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600

Qy 1533 GAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1592

Db 601 AGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660

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Qy 1653 TGTATCAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1691

Db 721 TGTATCAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 759

RESULT 6  
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LOCUS WHB3875\_G12\_M2325 wheat Fusarium graminearum infected spike cDNA  
DEFINITION library Triticum aestivum cDNA clone WHB3875\_G12\_M23, mRNA  
sequence.

ACCESSION CN010757

VERSION CN010757.1 GI:45800789

KEYWORDS EST.

SOURCE Triticum aestivum (bread wheat)

ORGANISM Triticum aestivum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; liliopsida; Poales; Poaceae;

REFERENCE 1 (bases 1 to 799)  
Anderson, O.D., Zhao, S., Han, P.S., Heinen, S., Hsia, C.C., Kang, Y., Kruger, W.M., Izzo, G.R., Miller, S., Muehlbauer, G.J., Miller, R., Pritsch, C., Rausch, C.J., Seaton, C.L., Tong, J.C., Vance, C. and Wilson, C.F.

AUTHORS The structure and function of the expressed portion of the wheat  
genomes - Fusarium graminearum infected spike cDNA library  
Unpublished (2001)

JOURNAL Contact: Olin Anderson

COMMENT US Department of Agriculture, Agriculture Research Service, Pacific  
West Area, Western Regional Research Center  
800 Buchanan Street, Albany, CA 94710, USA  
Tel: 5105595773  
Fax: 5105595818

Email: candersn@pw.usda.gov  
 Sequences have been trimmed to remove vector sequence and low quality sequence with phred score less than 20. No effort was taken to identify ESTs of fungal origin from this library, thus this EST could be of wheat or fungal origin.  
 Seq primer: SK primer.

## FEATURES

## SOURCE

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 /note="Vector: Lambda Uni-ZAP XR, excised phagemid pluscript SK; Site 1: EcoRI; Site 2: XhoI; Plants were grown in the greenhouse. Spikes were sprayed at anthesis with Fusarium graminearum. Total RNA, and poly(A) RNA were prepared and pooled from infected spike at 0, 6, 12, 24, 36 and 48 hours after inoculation, a cDNA library was made, and the cDNA clones were in vivo excised to give pluscript phagemids in G. Muehlbauer lab at the University of Minnesota (Krugler, W.M., Muehlbauer, G.J., Pritsch, C., Vance, C.). The cDNA library should contain genes of both wheat and fungal pathogen origin. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."

## ORIGIN

Query Match 22.5%; Score 438.2; DB 7; Length 799;  
 Best Local Similarity 72.9%; Pred. No. 5.8e-97;

Matches 577; Conservative 0; Mismatches 213; Indels 1; Gaps 1;

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 880 TTGCTAGTGGGAAAGAAAGTCTGTGAGCAGTTGAAAGTGGAGTGTGACGAGAG 939  
 68 CTGCTTAATGCAAGAGATGCTGTGAAGCAATGAACTGGGAGTGGCAGAGAG 127  
 940 AGGAGTTTCGAGAGGTGAGATCATGCGAGAGTTCACAGGCACTGTGTCT 999  
 128 CGTAGTTCGAGGAGGTGAGATTCACGCGTGTTCACACAGCACTGTGTCT 187  
 1000 CTTGTTGTTATTCATCGCCGCGTCCAAAAGATTGCTGTATGAGTTGTTCTTAAC 1059  
 188 CTGTTGGTTATCTGATCTCTGGGGGGAAGAGTTGCTGTATGAGTTGTTACCAAT 247  
 1060 AACAACTCCGAGCTTCACTCCATGCGGAGGAGCGCTTAATGAATGAGACCAAGA 1119  
 248 AACACATGGAATTCACCTTACATGAAAGCGGTCCAAAGTTGAGTGGCCATAGA 307  
 1120 TTGAAGATTGCTTGAATGCTGTAAGAGCTTCTTATCTTCAAGAGATTGCAATCT 1179  
 308 CTAAAGATGCTCTTGGTCTGCTTAAGGTTTGGCATTCATCAGAAAGATTGCCACCG 367  
 1180 AAAATCATTCACCGTATATCAAGGCTTCAAAATATTGATAGATTCAAGTTGAAGCT 1239  
 368 AAGATCATACATCGATATTAAGTCATCAACAATCTTCTTGAATTTAAATTGGAAGCT 427  
 1240 AAGTTGCTGATTTTGTCTTGAATGCTTCTTGAATTAACAACGCGATGATCAACA 1299  
 428 AAGGTTGGGAGTTTGTCTGCAAAAGTTCACTCTGATTAACAACACACAGTGTCAACA 487  
 1300 CGTGTGATGGAACTTTGGGACTTGGCTCGGAAATCGCTGCAAGGGGAAAGCTCAG 1359  
 488 AGAGTAATGGCACTTTTGGTATCTAGACCAAGATATGCGCTTCTTGGAAAGCTAATCT 547

QY 1360 GAGAGTCTGACGTTTTCTCATTTGGCGTGTGCTTTGGAGCTCATTAAGTCACTGCA 1419  
 DB 548 GAGAAATCAGATGCTTTCTTTGGATGATGCTTCTTGAAGTGAATTAAGTGGCGCGG 607  
 QY 1420 CCCGTGATGCCCAACATGCTCTATGATGAGACAGCTTATTTGACTGGGACAGCACTTG 1479  
 DB 608 CCGTTGATTTCAACCCCAACATATATGATGACAGCTGTGTTGATTTGGCAAGCCTTTTA 667  
 QY 1480 CTTAACCGAGCATCTGAGCAAGAGACTTTGAGGTTTACCTGATGCAAAAGATGATATAT 1539  
 DB 668 CTGATGAGACACTTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATG 727  
 QY 1540 GGGTATGACAGAGAGAGATGCTCGCATGCTGCTTGTGCTGCGGCTGTTGTTGCCAT 1599  
 DB 728 GATTTCATCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 787  
 QY 1600 TCAGCTGCGCG 1610  
 DB 788 TCAGCAGCTCG 798

## RESULT 7

## LOCUS

BS596561 757 bp mRNA linear EST 07-MAR-2003  
 EST495239 cSTS Solanum tuberosum cDNA clone cSTS15A23 5' sequence,  
 mRNA sequence.

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

Solanum tuberosum (potato)  
 Solanum tuberosum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 asterids; lamiales; Solanales; Solanaceae; Solanum.

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

The Institute for Genomic Research  
 9712 Medical Center Dr, Rockville, MD 20850, USA  
 Email: potato-array@tigr.org  
 This clone can be obtained from the University of Arizona Genomics  
 Institute. Orders can be made through URL:  
<http://genome.arizona.edu/orders/>  
 Seq primer: M13P-R.

## FEATURES

## SOURCE

1. 757  
 /organism="Solanum tuberosum"  
 /mol\_type="mRNA"  
 /cultivar="Kennebec"  
 /db\_xref="taxon:4113"  
 /clone="cSTS15A23"  
 /tissue\_type="sprouting eyes from tubers"  
 /dev\_stage="12-14 weeks post harvest"  
 /lab\_host="SOLR"  
 /clone\_lib="cSTS"  
 /note="Vector: pluscript SK(-); Site 1: EcoRI; Site 2: XhoI; Various sizes of sprouting eyes (2mm to 15mm) were taken from tubers. The tubers were incubated at 26C in the dark for 2-3 weeks prior to sprouting. The eyes were frozen in liquid nitrogen immediately upon removal from tubers."

## ORIGIN

Query Match 22.1%; Score 429.6; DB 4; Length 757;  
 Best Local Similarity 73.4%; Pred. No. 7.6e-95;

Matches 549; Conservative 0; Mismatches 199; Indels 0; Gaps 0;

QY 901 GCTGTGAACAGTGAAGTTGGGAGTGTGACGAGAGAGAGATTTCAGGACAGAGTT 960  
 DB 1 GCGTTAAACAGCTTAAGCTGAGAGTGAAGTGAACAGGAGAACTGAATTTCAAGCGGAAGTT 60

QY 961 GAGATCATCAGCAGAGTTCCACACAGCATCTGGTCTCTCTGTTGTTATGATCGCC 1020  
 Db 61 GAGATTTATTCAGCGAGTACATCACACATCTTGTCTCTTGTGATCTGATTAAT 120  
 QY 1021 GGTGCCAAAGATTGCTGTCTATGAGTTTGTCTTACAACAATCTGAGCTTCACTC 1080  
 Db 121 GGGGCTCAGAGACTGCTGTTTATGAGTTTGTCTTACAACAATCTTGGATTTCAATTA 180  
 QY 1081 CATGCGAGGAGCGGCTACATGAGATGAGACACAGATTTGAATGCTCTTGGATCT 1140  
 Db 181 CACGGAAGGAGAGGCTCTCTTGTGATGGCCATACGCTTAAGATGCTCTAGAGTCA 240  
 QY 1141 GCTAAAGACTTCTTATCTTCACTGAGATTTGCACTTAAATCACTTACCGTATATC 1200  
 Db 241 GCTAAAGACTGCTCAATCTGATGAGAGACTGCAACCGAAATCAATCACTGATATC 300  
 QY 1201 AAGGCTTCAACATATTGATGATTTCAAGTTTGAAGCTTGAAGTTTGGTCTT 1260  
 Db 301 AAGGCTTCAACATATTGATGATTTCAAGTTTGAAGCTTGAAGTTTGGTCTT 360  
 QY 1261 GCTAAGATGCTTCTGATACCAACAGCATGATATCAACAGTGTATGAGAACTTTGGG 1320  
 Db 361 GCTAAGATGCTTCTGATACCAACAGCATGATATCAACAGTGTATGAGAACTTTGGG 420  
 QY 1321 TACTTGGCTCCGGAATACGCTGCAAGCGGAAAGCTCAGGAGAGCTTGTATGCTT 1380  
 Db 421 TACTTGGCTCCGGAATACGCTGCAAGCGGAAAGCTTGTATGCTTGTATGCTT 480  
 QY 1381 TTTGGCTTGTCTTGTGAGCTCATTTACTGAGAGCTGACCCGTTGATGCCAACAATGTC 1440  
 Db 481 TTTGGCTTGTCTTGTGAGCTCATTTACTGAGAGCTGACCCGTTGATGCCAACAATGTC 540  
 QY 1441 TATGATGATGAGAGCTTGTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500  
 Db 541 TATGATGATGAGAGCTTGTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600  
 QY 1501 GAGAGCTTGAAGGCTTGTGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1560  
 Db 601 GAGAGCTTGAAGGCTTGTGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660  
 QY 1561 GCTGAGCTGTTGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1620  
 Db 661 GCTGAGCTGTTGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720  
 QY 1621 ATGAGCGAGATTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1648  
 Db 721 ATGAGCGAGATTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 748

RESULT 8  
 CB655196 731 bp mRNA linear EST 09-APR-2003  
 DEFINITION OSUNEC08F21.f OSUNEC Oryza sativa (japonica cultivar-group) cDNA  
 LOCUS CB655196  
 ACCESSION CB655196  
 VERSION CB655196.1 GI:29658921  
 KEYWORDS EST.  
 SOURCE Oryza sativa (japonica cultivar-group)  
 ORGANISM Oryza sativa (japonica cultivar-group)  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.  
 1 (bases 1 to 731)  
 Jantsauriyarat,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E.,  
 Kudrna,D., Dean,R., Soderlund,C., Wang,R. and Wang,G.  
 Large-scale identification of ESTs involved in the interaction  
 between rice and Magnaporthe grisea  
 Unpublished (2003)  
 CONTACT: Rod Wing  
 Arizona Genomics Institute  
 University of Arizona  
 Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ

85721-0088, USA  
 Tel: 520 626 3967  
 Fax: 520 621 9288  
 Email: http://genome.arizona.edu  
 PCR PRIMERS  
 FORWARD: gta aac cga cgg cca gtc  
 BACKWARD: gga aac agc tat gac cat g  
 Plate: 08 row: F column: 21  
 Seq primer: gta aac cga cgg cca gtc.  
 Location/Qualifiers  
 1. 731  
 /organism="Oryza sativa (japonica cultivar-group)"  
 /mol\_type="mRNA"  
 /cultivar="Nipponbare"  
 /db\_xref="taxon:39847"  
 /clone="OSUNEC08F21"  
 /issue\_type="leaf"  
 /dev\_stage="3 week"  
 /lab\_host="DH10B"  
 /clone\_1fb="OSUNEC"  
 /note="Vector: pBluescript II KS+; Site 1: EcoRI; Site 2:  
 XhoI; 6 hrs after inoculation with Rice Blast (C9240-1)"

ORIGIN  
 Query Match 21.6%; Score 419.2; DB 6; Length 731;  
 Best Local Similarity 73.5%; Pred. No. 2.8e-92;  
 Matches 535; Conservative 0; Mismatches 193; Indels 0; Gaps 0;

QY 931 CAGGAG 990  
 Db 1 CAGGAG 60  
 QY 991 CTGGTCTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1050  
 Db 61 CTGGTCTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 120  
 QY 1051 GTTCTTAAACAATCTGAG 1110  
 Db 121 GTTCTTAAACAATCTGAG 180  
 QY 1111 AGCAG 1170  
 Db 181 AGCAG 240  
 QY 1171 TGCAATCTTAAATCTTCAACAG 1230  
 Db 241 TGCAATCTTAAATCTTCAACAG 300  
 QY 1231 TTTGAAGCTAAGGTTGCTGATTTTGTCTTGTGCTAAGATGCTTGTGATTAACAACAGAGAT 1290  
 Db 301 TTTGAAGCTAAGGTTGCTGATTTTGTCTTGTGCTAAGATGCTTGTGATTAACAACAGAGAT 360  
 QY 1291 GTATCAACAGTGATGAG 1350  
 Db 361 GTTTCAGCAAGAGATGAG 420  
 QY 1351 AAGCTCAGGAG 1410  
 Db 421 AAGCTCAGGAG 480  
 QY 1411 GAGAGTGAACCCCTTGAATGCAACATGCTATGATGATGATGATGATGATGATGATGATGAT 1470  
 Db 481 GAGAGTGAACCCCTTGAATGCAACATGCTATGATGATGATGATGATGATGATGATGATGAT 540  
 QY 1471 CGAACATGCTTAAACGAG 1530  
 Db 541 AGGCTTTTACTGATGAG 600  
 QY 1531 ATGAATTAAGGATGATGAG 1590  
 Db 601 CTGGGAGAGAGATTTCAATCCCAATGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660  
 QY 1591 GTTTCGCAATTCAGCTGCGCAG 1650

DB 661 GTACCCGATTCGCTGCTGCTGCCACGCAAGAGCGAGTGTGCGGCTTGAAGGT 720  
QY 1651 AATGTATC 1658  
DB 721 GACGTGTC 728

RESULT 9  
CNSOAKU 2734 bp mRNA linear HTC 06-FEB-2004  
LOCUS Arabidopsis thaliana Full-length cDNA Complete sequence from clone  
DEFINITION GS1P6H5ZE04 of Hormone Treated Callus of strain col-0 of  
Arabidopsis thaliana (thale cress).  
ACCESSION BX816903.1 GI:42469997  
VERSION HTCC GSUT cDNA.  
KEYWORDS Arabidopsis thaliana (thale cress)  
SOURCE Arabidopsis thaliana  
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eustoids II; Brassicales; Brassicaceae; Arabidopsis.  
REFERENCE 1 (bases 1 to 2734)  
AUTHORS Castelli V., Aury J.M., Jallion O., Wincker P., Clepet C.,  
Menard M., Cruaud C., Quetier F., Scarpelli C., Schachter V.,  
Temple G., Caboche M., Weissenbach J. and Salanoubat M.  
Whole Genome Sequence Comparisons and 'Full-length' cDNA Sequences:  
A Combined Approach to Evaluate and Improve Arabidopsis Genome  
Annotation  
Unpublished  
JOURNAL 2 (bases 1 to 2734)  
REFERENCE Genoscope.  
AUTHORS Direct Submission  
JOURNAL Submitted (18-NOV-2003) Genoscope - Centre National de Sequenage :  
BP 191 91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr  
COMMENT - Web : www.genoscope.cns.fr)  
The sequences are based on single pass reads.  
Life Technologies (a division of Invitrogen) members carried out  
full-length libraries construction : Temple G.  
Genoscope members carried out sequencing and annotation : Castelli  
V., Aury J.M., Jallion O., Wincker P., Menard M., Cruaud C.,  
Schachter V., Weissenbach J., Salanoubat M.  
URV INRA : Clepet C., Caboche M.  
Annotation is based on the June 2003 version of the Arabidopsis  
genome released by MIPS (Munich Information center for Protein  
Sequences). 5 prime and 3 prime are assembled with Phrap.  
http://www.genoscope.cns.fr/externe/sequences/Banque\_Projet\_EF/Full  
length  
http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis.  
FEATURES  
SOURCE Location/Qualifiers  
1..2734  
/organism="Arabidopsis thaliana"  
/mol\_type="mRNA"  
/strain="Col-0"  
/db\_xref="taxon:3702"  
/clone="GS1P6H5ZE04"  
/tissue\_type="Hormone Treated Callus"  
/plasmid="PCMVSPORT\_6"  
1..2734  
/gene="At1g70460"

ORIGIN  
Query Match 21.5%; Score 417.6; DB 3; Length 2734;  
Best Local Similarity 64.0%; Pred. No. 9.3e-92;  
Matches 678; Conservative 0; Mismatches 354; Indels 28; Gaps 2;

QY 763 GTGTAGGCTTCCTCCAAAGCACTTTCACATACGAGAGCTAGAGCCACCAATGCT 822  
DB 1306 GTGATGGGAAGTGTCAACACATTTCAATATGAAGAGCTAACGAGCATACAGAGGA 1365  
QY 823 TTCTCGAGGCAACTTGTAGACAGAGCGGCTTGGTTACGTGACAAAGGTGCTTG 882  
DB 1366 TTTTCAAGCATTAACATCTTGGAGAGAGGTTTGTGTGTATTAAGGTAAATTA 1425

QY 883 CCTAGTGGAAAGAACTGTGTGTGAAGCAATTGAAAGTTGGAGATGTGTGAGGAGAG 942  
DB 1426 AATGATGGAAACTTGTGTGTGTGTGAAGCACTTAAGTTGGAGAGAGAGTACCT 1485  
QY 943 GAGTTTCAGGAGAGAGTGAATGATGATGATGATGATGATGATGATGATGATGAT 1002  
DB 1486 GAGTTTAAAGCGAGAGTGAATGATGATGATGATGATGATGATGATGATGATGAT 1545  
QY 1003 GTTGTATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1062  
DB 1546 GTTGTATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1605  
QY 1063 AATTCGAGCTTCACTTCATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1122  
DB 1606 ACATGGAACATCATTTGATGATGATGATGATGATGATGATGATGATGATGAT 1665  
QY 1123 AAGATGCTCTTGGATCTGCTAAAGAGCTTCTTATCTCATGAAAGTTGCAAT 1182  
DB 1666 AGAATGCTATAGTCTGCTGCAAGAGTTGGCGTATTATACAGAAAGCTGTAC 1725  
QY 1183 ATCATTCACGCTGATATCAAGGCTTCAACATATGATGATTTCAAGTTGAAGT 1242  
DB 1726 ATCATTCACGCTGATATCAAGGCTTCAACATATGATGATTTCAAGTTGAAGT 1785  
QY 1243 GTTGTGATTTTGTGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1302  
DB 1786 GTTGTGATTTTGTGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1845  
QY 1303 GTGATGGGAACCTTTGGGCTACTTGGCTCCGAAATACGCTCAAGCGGAAAG 1362  
DB 1846 GTTATGGGAACCTTTGGGCTACTTGGCTCCGAAATACGCTCAAGCGGAAAG 1905  
QY 1363 AAGCTGACGCTTTCTGATTTGGGCTTTGCTTTGAGCTCATTTACGAGCTGAC 1422  
DB 1906 AGATTCAGATGTTTCTGTTGGGCTTTGCTTTGAGCTCATTTACGAGCTGAC 1965  
QY 1423 GTTGTATCCCAATATGCTATGATGATGATGATGATGATGATGATGATGATGAT 1482  
DB 1966 GTTGTATCCCAATATGCTATGATGATGATGATGATGATGATGATGATGATGAT 2025  
QY 1483 AACGAGCATCTGAGCAAGAGAGCTTTGAGGCTTGAAGTGAATGAATGAATGAG 1542  
DB 2026 CACAAAGCATTTGAGACCGGATTTTCACTGATGATGATGATGATGATGATGAT 2085  
QY 1543 TATGACAGAGAGAGATGCTGATGATGATGATGATGATGATGATGATGATGAT 1601  
DB 2086 TATGACAGAGAGATGCTGATGATGATGATGATGATGATGATGATGATGAT 2145  
QY 1602 AGCTGCGCGAGAGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1661  
DB 2146 AGCTGCGCGAGAGCTGATGATGATGATGATGATGATGATGATGATGATGAT 2205  
QY 1662 GTGATGCTTAAAGAGAGATGATGATGATGATGATGATGATGATGATGATGAT 1721  
DB 2206 GAGAGATATCAAGCAATGATGATGATGATGATGATGATGATGATGATGAT 2245  
QY 1722 AAGCAGCATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1781  
DB 2246 -----GCTTATGATCTGCTGATGATGATGATGATGATGATGATGATGAT 2298  
QY 1782 ACTTGAAGTCAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1821  
DB 2298 ATTGTGTTTGAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 2338

RESULT 10  
BG441204 692 bp mRNA linear EST 15-MAR-2001  
LOCUS BG441204  
DEFINITION GA\_Ea0012C15f Gossypium atboreum 7-10 dpa fiber library  
arborescens cDNA clone GA\_Ea0012C15f, mRNA sequence.  
ACCESSION BG441204  
VERSION BG441204.1 GI:13350856



KEYWORDS EST.  
SOURCE Gossypium arboreum  
ORGANISM Gossypium arboreum  
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.  
AUTHORS Wing, R.A., Frisch, D., Yu, Y., Main, D., Ramo, T., Simmons, J., Henry, D., Wood, T.C., Leslie, A. and Wilkins, T.A.  
TITLE An integrated analysis of the genetics, development, and evolution of the cotton fiber  
JOURNAL Unpublished (2000)  
COMMENT Contact: Wing RA  
Clemson University Genomics Institute  
Clemson University  
100 Jordan Hall, Clemson, SC 29634, USA  
Tel: 864 656 7288  
Fax: 864 656 4293  
Email: rwing@clemson.edu  
Seq primer: TAATACGACTCACTATAGG  
High quality sequence stop: 690.  
Location/Qualifiers  
1. .692  
/organism="Gossypium arboreum"  
/mol\_type="mRNA"  
/strain="AKA"  
/cultivar="8400"  
/db\_xref="taxon:29729"  
/clone="GA\_Ea0012C15f"  
/tissue\_type="Fibers isolated from bolls harvested 7-10 dpa"  
/lab\_host="E. coli"  
/clone\_lib="Gossypium arboreum 7-10 dpa fiber library"  
/note="Vector: pBK-CMV; Site\_1: EcoRI; Site\_2: XhoI"

ORIGIN

Query Match 21.3%; Score 413.2; DB 4; Length 692;  
Best Local Similarity 75.4%; Pred. No. 8.4e-91;  
Matches 514; Conservative 0; Mismatches 168; Indels 0; Gaps 0;

QY 739 CTTCCTCCACCGTCTCCAGGGCTGTGTAGCTTCCAAAGACCTTTCACATACAG 798  
DB 11 CTTCGGCTGCTACCTCGTATTTCTTAGGTTCTGAAAGACCTTTAGCTATGAA 70  
QY 799 GAGCTAGTAGAGCCCAATGTTCTCCAGGCGAATCTTGTAGCAAGCGCGGCTC 858  
DB 71 GAATTAAGTAGAGCAAGCGATGCTTCTCGAAGTTAACTTTGTAGCAAGGCTGTTT 130  
QY 859 GGTACGTGCAAAAGCTGTGCTTCTAGTGGAAAGAGTTGCTGAGCAGTTGAA 918  
DB 131 GGGTACGTACAAAGAGATTTCTCCTAATGGAAAGAGTAGCAAGTAAAGCACTCAG 190  
QY 919 GTTGGAGTGGTCAAGGAGAGAGAGATTTCAGGCAAGGTTGATCATCAGAGATT 978  
DB 191 GCTGGAGTGGGCAAGGCGAAGAGATTTCAGGCTGAAGTTGATCATTAAGTCCGCTC 250  
QY 979 CACCAAGGATCTGTGTCTTGTGTGTATTCATGCGCGGTGCCAAAGATTGCTT 1038  
DB 251 CATCAAAACATCTCGTCTCATTTGTCGATCTGTAATTTCTGGGAAATAAAGATGCTT 310  
QY 1039 GTCTAAGATTGTTCTTAAACAATCTGAGCTTCACTCCATGCGAGGAGCGGCT 1098  
DB 311 GTTTAAGATTGTTCTTAAACAACACTTGAAGTTCACTTGATGGGAAGGCGGCTG 370  
QY 1099 ACAATGGAATGAGCAACGATGGAAGATTGCTTGAATCTGTAAGACTTTCTTAT 1158  
DB 371 ACATGATTTGGCCGCAAGAGAGAAATTTGCTTTAGATCTGCAAAAGAGCTGCATAT 430  
QY 1159 CTTTCATGAAGATTGCAATCTTAAATCATTCACCGGATATCAAGGCTTCAACATATTG 1218  
DB 431 CTTTCATGAAGATTGCTATCTTAAGATCTTCAACCGGATATTAAGGCGCTTAATATTG 490  
QY 1219 ATAGATTTCAGATTGAAGCTAAGGTTGCTGATTTGCTTGTCTAAGATTGCTTCTGAT 1278

DB 491 TTGATTTCAAGTTTGAAGCAAAAGTTGCTGATTTTGACTAGCGAAATATGCTTCGAT 550  
QY 1279 ACAACAGCATGATATTAACACGTTGATGGAACTTTGGGTACTTGCTCCGAAATAC 1338  
DB 551 GTCAACAGCAGCTTCTCCACCGGTGATGGTACTTTCGGGTATTAGCCCTGAGATAT 610  
QY 1339 GCTGCAAGCGAAAGCTCAAGAGAGTCTGAGCTTTCTTCATTTGCGCTGTTTG 1398  
DB 611 GCTTCAAGTGAAGAAAGCTCACTGTAATATCAGATGTTTTCCTTCGGGTCATGCTTTG 670  
QY 1399 GAGCTATTACTGAGCTGCAC 1420  
DB 671 GAGTGTATTACCGTCAAGAC 692

RESULT 11  
AV543493/C  
LOCUS AV543493 584 bp mRNA linear EST 20-FEB-2004  
DEFINITION AV543493 Arabidopsis thaliana roots Columbia Arabidopsis thaliana  
ACCESSION AV543493  
VERSION AV543493.1 GI:8714907  
KEYWORDS EST  
SOURCE Arabidopsis thaliana (thale cress)  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
REFERENCE Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.  
A large scale analysis of cDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries  
DNA Res. 7 (3), 175-180 (2000)  
JOURNAL MEDLINE  
PUBMED 20363093  
COMMENT Contact: Erika Asamizu  
The First Laboratory for Plant Gene Research  
Kazusa DNA Research Institute  
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan  
Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.  
Location/Qualifiers  
1. .584  
/organism="Arabidopsis thaliana"  
/mol\_type="mRNA"  
/ecotype="Columbia"  
/db\_xref="taxon:3702"  
/clone="R2201f07F"  
/tissue\_type="roots"  
/clone\_lib="Arabidopsis thaliana roots Columbia"  
/note="Vector: pBluescriptII SK-; Site\_1: EcoRI; Site\_2: XhoI"

ORIGIN

Query Match 21.2%; Score 411.6; DB 1; Length 584;  
Best Local Similarity 90.9%; Pred. No. 2e-90;  
Matches 438; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 1463 ACTGGGACAGACCATGCTTTAACCGAGCATCTGAGCAAGAGACTTGAAGGCTTTAGCT 1522  
DB 584 ACTGGGACAGACCATGCTTTAACCGAGCATCTGAGCAAGAGACTTGAAGGCTTTAGCT 525  
QY 1523 ATGCAAGATGGAATATGAGTATGACAGAGAGAGATGCTGCGATGTTGCTTGCTG 1582  
DB 524 ATTCAAAGATGGGTAATGAGTATGACAGAGAGAGATGCTGCGATGTTGCTTGCTG 465  
QY 1583 CGGCTTGTGCGCATTCAGCTCGCGGAGACCTCGCATGAGCCGATTTGCGTGGCTG 1642  
DB 464 CGGCTTGTGCGCATTCAGCTCGCGGAGACCTCGCATGAGCCGATTTGCGTGGCTG 405  
QY 1643 TGAAGGAATATATCACTGTGATCTTTAAGAAAGGATGAGACCGAGGTCAAGCAATG 1702



Db 404 TAGAGAAATGATGCTGCTGTCTGATCTTAAAGAAAGGATGAGACCGGGTCAACCAACG 345  
 QY 1703 TATACAGCTCATACGAGAGAAAGCAACCGATTATGACTCGAGCCAGTCAATGAAGCATGA 1762  
 Db 344 TATACAGCTCATATGAGAGAAACAGACATATGACGAGCCAAATACAGACGACATGA 285  
 QY 1763 AGAAGTTTAGAAAAATGCGACTTGGAACTCCAGAGTACAGACGCGGTGAGTACAGTA 1822  
 Db 284 TAAAGTTTAGAAAAATGCGCTCTTGGAACTCAAGAAATACGCGACACACCGCGAGTACAGTA 225  
 QY 1823 ATCCGACCGAGTACGCTGAGTACGCTGCTGCTTCAAGCAGCGAGGCGCAACACACAC 1882  
 Db 224 ATCCACCGAGTACGCTGAGTACGCTGCTGCTTCAAGCAGTGAAGTCAAGCCACACAC 165  
 QY 1883 GCGAAATGAGATGCGGAAAGATTAGAGAACCGGTGAGGTTTATGAGACCTTCTCTT 1942  
 Db 164 GAGAAATGAGATGCGGAAAGATTAGAGAAACCGGTGAGGTTTATGAGACCTTCTCTT 105  
 QY 1943 AA 1944  
 Db 104 AA 103

RESULT 12  
 CFA36437 788 bp mRNA linear EST 04-SEP-2003  
 LOCUS CFA36437  
 DEFINITION EST672782 normalized cDNA library of onion Allium cepa cDNA clone  
 ACACM44, mRNA sequence.

ACCESSION CFA36437  
 VERSION CFA36437.1 GI:34459127  
 KEYWORDS EST  
 SOURCE Allium cepa (onion)  
 ORGANISM Allium cepa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Alliaceae;  
 Allium.

REFERENCE 1 (bases 1 to 788)  
 AUTHORS Havey, M.J., Cheung, F., Van Aken, S., Uteback, T. and Town, C.D.  
 TITLE Expressed Sequence Tags from a normalized library of mixed onion  
 tissues (Allium cepa)  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Havey MJ  
 Department of Horticulture  
 USDA-ARS and University of Wisconsin  
 1575 Linden Drive, Madison, WI 53706, USA  
 Tel: 608-262-1830  
 Fax: 608-262-4743  
 Email: mjhavy@facstaff.wisc.edu  
 TIGR sequence name ACACM44.1. For more information:  
 http://haveylab.hort.wisc.edu  
 Seg primer: CAG GAA ACA GCT ATG ACC.  
 Location/Qualifiers

FEATURES  
 source 1..788  
 /organism="Allium cepa"  
 /mol\_type="mRNA"  
 /cultivar="Red Creole (bulbs), unknown (callus), Epano &  
 Texas Legend (roots)"  
 /db\_xref="taxon:4679"  
 /clone="ACACM44"  
 /cistype="Callus, roots, and young bulbs"  
 /cistype="normalized cDNA library of onion"  
 /note="Vector: PCWMSport6.1-ccdb (Invitrogen); Site 1:  
 EcoRV (5'); Site 2: NotI (3'); Equal molar amounts of mRNA  
 from callus, roots, and young bulbs were combined to  
 synthesize the library. Normalization to enrich for  
 low-copy transcripts was performed by proprietary  
 techniques of Invitrogen."

## ORIGIN

Query Match 21.1%; Score 409.4; DB 7; Length 788;  
 Best Local Similarity 70.0%; Pred. No. 7.5e-90;  
 Matches 551; Conservative 0; Mismatches 236; Indels 0; Gaps 0;

QY 778 AAAAGCACTTCACTACGAGAGCTAGCTAGAGCCACCAAGGTTTCTCCAGGCAAC 837  
 Db 2 AAGAGCACTTCACTATGAGAAATGGCGAGTCAAAATGGTTTCCGACTATAT 61  
 QY 838 TTGTTAGGCAAGAGGCGGTTCGTTACGTGCAAAAGTGTGTTCCATGAGGAAAGA 897  
 Db 62 CTTCTTGGGCAAGTGTGATTTGGATATGTGCAAAAGGATCTTCAAAACGGTAAAGAA 121  
 QY 898 GTTGTGTGAGACAGTTGAAAGTTGGAGTGTCAAGGAGAGAGGAGTTTCAAGGACAG 957  
 Db 122 GTGGCTATCAACAGTGTGAAGCCGAGACGAGCAAGAGGAGGTGATTTCAAGACAG 181  
 QY 958 GTTGAATATATAGACAGAGTTCACCAAGCATCTGTGCTCTTGTGTTGATTTGATC 1017  
 Db 182 GTTGAATATATAGAGTGTGATTCATAGGATTTGTTTCTTATGTTGCTATTCAT 241  
 QY 1018 GCGGATGCCAAAGATTTGCTTCTATGAGTTGTTCTTCAACAATCTCGAGCTTAC 1077  
 Db 242 TCGAGGATCATAGATTGCTTCTTATGAAATATGTTCTTAAATAAACCTTGAAGTTCCAT 301  
 QY 1078 CTCATGCGGAGGAGCGCTTACATGGAATGAGACCAACGATGGAATGCTCTTGA 1137  
 Db 302 TTGCATGAAAAGATGTTCCACCTATGAGATTGCGCAACGCGTTTAAATTTGCTTGGT 361  
 QY 1138 TCTGCTAAAGACCTTCTTATCTTCAAGATTCATCTTAAATCATTCACCTGAT 1197  
 Db 362 TCTGCCAAGGCGTTGGCATATCTCCATGAGATTTGTATCCAAATATTCATCGTAT 421  
 QY 1198 ATCAAGGCTTCAAAATATGATGATTTCAAGTTGAAGCTTAAAGTTGCTGATTTGGT 1257  
 Db 422 ATTAAAGCAGCAATATCTTCTTGAATGATGAACTTGAAGCTTAAAGTTTGGC 481  
 QY 1258 CTTGCTAAGATTGCTTCTGATACAAACGAGATTCACACGTTGATGAGGAACTTT 1317  
 Db 482 CTTCAAAAGTTCACTGTGTGAATTAACACCATTTCTTACAGAGTCATGGAACATTT 541  
 QY 1318 GGTGACTTGGCTCGGAAATATGATGATTCGCAACGAAAGCTCAGGAACTGACGTTTC 1377  
 Db 542 GGTGATCTGGACAGAAATATGATTCCTCTGTAACGTAATGATGATGATGATGAT 601  
 QY 1378 TCATTTGCGCTTGTGCTTGTGAGTCACTTACTGACGTCGACCGTTGATGAGCAACAT 1437  
 Db 602 TCATTTGAGTCATGCTTGTGAGTGTATCTGGAAGGCAACGTTGATGCAACCA 661  
 QY 1438 GTCTATGATGATGACAGCTTGTGATGATCTGGGAGAGACCATGCTTAAACGACATCTGAG 1497  
 Db 662 ACTTATACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 721  
 QY 1498 CAAGGAGCTTTGAGGTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1557  
 Db 722 CATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 781  
 QY 1558 ATGCGTC 1564  
 Db 782 ATGCGAC 788

RESULT 13  
 BPI84771 1084 bp mRNA linear EST 17-JUL-2003  
 LOCUS BPI84771  
 DEFINITION BPI84771 pms rice panicle cDNA, germ cell generating stage Oryza  
 sativa (japonica cultivar-group) cDNA, mRNA sequence.  
 ACCESSION BPI84771 GI:32948199  
 VERSION BPI84771  
 KEYWORDS EST  
 SOURCE Oryza sativa (japonica cultivar-group)  
 ORGANISM Oryza sativa (japonica cultivar-group)  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Eriatoidae; Oryzaceae; Oryza.  
 REFERENCE 1 (bases 1 to 1084)  
 AUTHORS Moriguchi, K., Ito, Y., Yamazaki, Y. and Kurata, N.  
 TITLE Finding of various plant nuclear proteins using yeast nuclear

JOURNAL  
Unpublished (2003)  
Contact: Kazuki Moriguchi

Plant Genetics  
National Institute of Genetics

Vata 1111, Mishima, Shizuoka 411-8540, Japan  
Tel: 81-55-981-6872  
Fax: 81-55-981-6879

Email: kmoriguc@lab.nig.ac.jp

cDNA clone obtained from nuclear transportation trap system  
encoding a protein similar to Oryza sativa (Japanese  
cultivar-group) putative receptor protein kinase PERK1.  
Location/Qualifiers

# FEATURES

source

1. 1084

/organism="Oryza sativa (Japanese cultivar-group)"

/mol\_type="mRNA"

/db\_xref="taxon:39947"

/issue\_type="panicle"

/dev\_stage="germ cell generating stage"

/clone\_lib="PNS rice panicle cDNA, germ cell generating stage"

## ORIGIN

Query Match

21.0%; Score 408.6; DB 5; Length 1084;

Best Local Similarity 69.3%; Pred. No. 1.3e-89;

Matches 587; Conservative 0; Mismatches 254; Indels 6; Gaps 2;

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Db 1137 ATCTGCTAAAGGACTTTTATCTTCATGAAGATTTGACATCTTAAATTCATCACCCTGA 1196
Oy 61 AGCTCAAGGCTTTAGCTTATCTTCATGAAGATTTGACATCTTAAATTCATCACCCTGA 120
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Oy 1197 TATCAAGCTTCAACATATTTGATTTGAAAGTTCAGTTGATTTGG 1256
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Oy 1257 TCTTGCTAAGATTTGCTTCTGATTAACAACGCTATATCAACGCTGATTTGG 1316
Db 181 ACTTGCTAAGATTTGCTTCTGATTAACAACGCTATATCAACGCTGATTTGG 1316
Oy 1317 TGGGTAAGCTTGGCTCGGAAATGAGCTGCAAGGCGAAAGCTCGAGAGTCTGAGTTT 1376
Db 241 TGGATATCTACACCAAGAGTACGATCTTCTGCAAGCTCCTAGAAATGATTTGCTT 300
Oy 1377 CTGATTTGGCGTGTGCTTTTGAAGCTCATTACTGAGCTGACCGCTTGAATGCAACA 1436
Db 301 CTGATTTGGCGTGTGCTTTTGAAGCTCATTACTGAGCTGACCGCTTGAATGCAACA 1436
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Db 361 AACATATATGATATACAGCTTATTTGACTGGGCAAGCAATTTGCTTAAACGAGATCTGA 1496
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Db 421 GAATGATACAGAGAGATTTAGATTTGAGATCTTCTGCGCTTGGAGAGATTTCAATCCCAATGA 480
Oy 1557 GATGGCTGCGATGCTTCTGCTGCTGCGCTTGTGCTTGGCATTCAGCTGCGCGCAGACC 1616
Db 481 GATGGCTGCGATGCTTCTGCTGCTGCGCTTGTGCTTGGCATTCAGCTGCGCGCAGACC 1616
Oy 1617 TCGCATGAGCAGATTTGCGGCTTGAAGAGAAATGATTTCACTGTCAGATTTTAAAGA 1676
Db 541 ACCGATGAGCAGATTTGCGGCTTGAAGAGAAATGATTTCACTGTCAGATTTTAAAGA 1676
Oy 1677 AGGAGTGAAGCAGCTCAAGCAATGATATACAGCTTAAAGAGAGAGAGAGAGAGAGAGAG 1736
Db 601 AGGAGTGAAGCAGCTCAAGCAGCTTATTTGATTTGATTTGATTTGATTTGATTTGATTTG 657
Oy 1737 CTGAGCAGATTAATGAGAGATTTAGAGAAATGCAATTTGGAATCTCAGA 1796

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Db 715 TATGATACAGAGATGATATACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 774

Oy 1857 TTCAACAGCAG 1916

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Oy 1917 TCAAGGT 1923

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RESULT 14  
CP436655 789 bp mRNA linear EST 04-SEP-2003

LOCUS EST673000 normalized cDNA library of onion Allium cepa cDNA clone

DEFINITION ACCK26, mRNA sequence.

ACCESSION CP436655

VERSION CP436655.1 GI:34459345

KEYWORDS EST

SOURCE Allium cepa (onion)

ORGANISM Allium cepa

REFERENCE 1 (bases 1 to 789)  
Hayes, M.J., Cheung, F., Van Aken, S., Uteback, T. and Town, C.D.

Expressed Sequence Tags from a normalized library of mixed onion

tissues (Allium cepa)

Unpublished (2003)

Contact: Hayes MJ

Department of Horticulture

USDA-ARS and University of Wisconsin

1575 Linden Drive, Madison, WI 53706, USA

Tel: 608-262-1830

Fax: 608-262-4743

Email: mjhayes@facstaff.wisc.edu

TIGR sequence name ACCK26. For more information:

http://hayeslab.hort.wisc.edu

Seq primer: CAG GAA ACA GCT ATG ACC.

Location/Qualifiers

1. 789

/organism="Allium cepa"

/mol\_type="mRNA"

/cultivar="Red Creole (bulbs), unknown (callus), Ebano &

Texas Legend (roots)"

/db\_xref="taxon:4679"

/clone="ACCK26"

/issue\_type="Callus, roots, and young bulbs"

/clone\_lib="normalized cDNA library of onion"

/note="Vector: pCMVSPORT6.1-cdb (Invitrogen); Site 1:

EcoRV (5'); Site 2: NotI (3'); Equal molar amounts of mRNA

from callus, roots, and young bulbs were combined to

synthesize the library. Normalization to enrich for

low-copy transcripts was performed by proprietary

techniques of Invitrogen."

## ORIGIN

Query Match

20.9%; Score 405.6; DB 7; Length 789;

Best Local Similarity 69.7%; Pred. No. 6.5e-89;

Matches 549; Conservative 0; Mismatches 239; Indels 0; Gaps 0;

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Oy 778 AAAAGCACTTTCATATGAGAGAGCTAGTAGCAACCAATGTTTCTCGAGCGAAC 837
Db 2 AAGAGCACTTTCATATGAGAGAGCTAGTAGCAACCAATGTTTCTCGAGCGAAC 837
Oy 838 TTGTAAGCAAGGCGGTTGCTTACGTCACAAAGGTGTGTTGCTTGTGGAAGAA 897
Db 62 CTCTTGGCGAGGTGATTTGATATGTGCAAAAGGATCTTCCAAACGGTAAGAA 121

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QY 898 GTTGTCTGTAAGACAGTGAAGTGGAGTGTGTCAGGAGAGAGAGGAGTTTCAGCAGAG 957  
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 QY 958 GTTGAGATCATCAGCAGAGTTCACGACAGCATCTGGTCTCTTGTGGTTATTCATC 1017  
 Db 182 GTTGAATTTATCAGTGAAGTGCATGATGATGATGATGATGATGATGATGATGATGAT 241  
 QY 1018 GCGCGTCCAAAAGATTTGCTGTCTTATGAGTTTGTCTTAAACAACAATCTGAGCTTAC 1077  
 Db 242 TCAGGAGATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 301  
 QY 1078 CTCGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1137  
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 Db 422 ATTAAGCAGCAAAATTTCTTCTTGAATGATGATGATGATGATGATGATGATGATGATGAT 481  
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 QY 1318 GGGTACTTGGCTCGGAAATACGCTGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1377  
 Db 542 GGGTACTTGGCTCGGAAATACGCTGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 601  
 QY 1378 TCATTTGGCGTTGCTGCTTGTGAGCTTATTAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1437  
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 QY 1438 GTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1497  
 Db 662 ACTTATACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 721  
 QY 1498 CAAAGGAGCTTGGAGGTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1557  
 Db 722 CATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 781  
 QY 1558 ATGGCTCG 1565  
 Db 782 ATGGCAGC 789

RESULT 15  
 CN816079 827 bp mRNA linear EST 18-JUL-2004  
 LOCUS HR04516.F12.L24255.L1b.AA071E1X.Avena sativa cv. Ogle-C root Avena  
 DEFINITION sativa cDNA clone HR04516.F12.L24, mRNA sequence.  
 ACCESSION CN816079  
 VERSION CN816079.1 GI:50357439  
 KEYWORDS EST.  
 ORGANISM Avena sativa (oat)  
 SOURCE Avena sativa  
 ORGANISM Avena sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Pooideae; Aveneae; Avena.  
 1 (bases 1 to 827)  
 Rines, H.W., Anderson, O.D., Crossman, C.C., Lazo, G.R., Miller, S.S.,  
 Tallier, J.M., and Vance, C.P.  
 ESTs from Avena sativa cv. Ogle-C roots, etiolated leaves, and  
 green leaves  
 Unpublished (2004)  
 Contact: Rines, H.W.  
 USDA-ARS and University of Minnesota  
 1991 Upper Buford Circle, 411 Borlaug Hall, St. Paul, MN 55108, USA  
 Tel: 612 625 5220  
 Fax: 612 625 1268

Email: rines001@umn.edu  
 Sequences have been trimmed to remove low quality sequence with  
 phred scores less than 20 and most vector sequence.  
 Seq primer: SK-5prime.  
 Location/Qualifiers  
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 (sequencing)"  
 /clone="lib AA071E1X Avena sativa cv. Ogle-C root"  
 /note="Vector: Lambda Uni-ZAP XR, excised phagemid;  
 Site 1: EcoRI; Site 2: XhoI; Seed were germinated in a  
 dark incubator at 20 C. At 6 days roots were harvested,  
 total RNA and poly(A) were prepared, a cDNA library was  
 made, and the cDNA clones were in vivo excised to give  
 phagescript phagemids in the Hw Rines and CP Vance  
 USDA-ARS labs (Rines, Vance, Miller, Tallier) at the  
 University of Minnesota, St. Paul, MN. Plasmid DNA  
 preparations and DNA sequencing were performed in the OD  
 Anderson USDA-ARS lab (Anderson, Crossman, Lazo) in  
 Albany, CA.  
 TAG\_TISIDE=root  
 TAG\_L1B=AA071E1X"

## ORIGIN

Query Match 20.8%; Score 403.8; DB 7; Length 827;  
 Best Local Similarity 70.0%; Pred. No. 1.8e-88;  
 Matches 559; Conservative 0; Mismatches 237; Indels 3; Gaps 1;

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 Db 71 ACATTTGGAAATTCACCTTACATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 130  
 QY 1123 AAGAATGCTTGGATGCTGTAAGGACTTCTTATCTTCAATGAGGAGGAGGAGGAGGAGGAG 1182  
 Db 131 AGGATGCTCTTGGTGGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 190  
 QY 1183 ATCATTCACGCGATATCAAGGCTTCAACATATGATGATGATGATGATGATGATGATGATGAT 1242  
 Db 191 ATATATACATCGATATTAAGTCAATCAACATTCCTTGAATTTAAATTTGAAGCCAG 250  
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 Db 371 AAGTCAAGCTTTTCTCATTTGGCGTGTGCTTTTGAAGCTCATTAATGAGGAGGAGGAG 430  
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 Db 491 ATGCGAGCATCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 550  
 QY 1543 TATGACAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1602

Db 551 TTCAATCTTAATGATAGATAGCCAGATGATAGCGTGTGCGCGCGCATGTGTACGCCATTCT 610  
 QY 1603 GCTGCGCGCAGACCTCGCATGAGCCAGATTGTGCGTCCGTTAGAAAGAAATGTATCACTG 1662  
 Db 611 GCAAGCGCGTGCACAGATGATGAGTGTGCGGCTTGGAAAGGTGACGTGTCTTTG 670  
 QY 1663 TCAGATCTTAACGAAGGATGAGACCGATCAAGCAATGTATACGCTCATACGAGGA 1722  
 Db 671 GAAGATCTTAACGAAGGTGTTCGGCTTGCCATAGCCGCTTCTTTGATGTAC--AGC 727  
 QY 1723 AGCACCATTATGATCTGAGCCAGTACATGAAGACATGAAGAAGTTAGAAATGCA 1782  
 Db 728 AGTTCGACTACGATTCTGACAGTATAACGAGACATGAAGAAAGTTCAGAAAGATGGCT 787  
 QY 1783 CTGGAAGTCAAGAGTACA 1801  
 Db 788 TTACGACGACGACTACA 806

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 Job time : 4172 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Comugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 13, 2004, 10:58:35 ; Search time 5549 Seconds

(without alignments)  
16567.161 Million cell updates/sec

Title: US-10-069-304-1  
Perfect score: 1944

Sequence: 1 atgctctgcgcgcgcgtctcc.....atagcgacctctctctta 1944

Scoring table: OLIGO\_NTC  
Gapco 60.0 , Gapext 60.0

Searched: 4526729 seqs, 23644849745 residues

Word size : 0

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database :

GenBank1:\*  
1: gb\_ba:\*  
2: gb\_hig:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pal:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_str:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vl:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	* Match Length	ID	Description
1	1944	100.0	1944 6 AX088876	AX088876 Sequence
2	1944	100.0	1944 6 AX825703	AX825703 Sequence
3	1944	100.0	1944 6 AX825705	AX825705 Sequence
4	1944	100.0	1944 6 AX028699	AX028699 Brassica
5	66	3.4	668 8 AY536856	AY536856 Arabidops
6	66	3.4	1959 6 AX825738	AX825738 Sequence
7	66	3.4	1959 8 BT008400	BT008400 Arabidops
8	66	3.4	1959 8 BT008409	BT008409 Arabidops
9	66	3.4	2098 8 AY128792	AY128792 Arabidops
10	66	3.4	2116 8 AY056788	AY056788 Arabidops
11	66	3.4	2188 8 AY059901	AY059901 Arabidops
12	66	3.4	2190 8 AY093065	AY093065 Arabidops
13	66	3.4	2257 8 AF370509	AF370509 Arabidops
14	66	3.4	2257 8 AB020746	AB020746 Arabidops
15	47	2.4	2324 8 AY089024	AY089024 Arabidops
16	29	1.5	80393 8 AP000382	AP000382 Arabidops
17	26	1.3	1515 6 AX825736	AX825736 Sequence
18	26	1.3	47428 6 AX059540	AX059540 Sequence
19	26	1.3	106977 2 AC124968	AC124968 Medicago

20	1.3	145453	8	AC012477	AC012477 Genomic S
21	1.3	183147	8	AC012392	AC012392 Genomic S
22	1.3	199987	8	ATCHR15	ATCHR15
23	1.2	898	8	AK109201	AK109201 Oryza sat
24	1.2	1389	6	AK654306	AK654306 Sequence
25	1.2	1922	8	AK070323	AK070323 Oryza sat
26	1.2	147516	8	AP004622	AP004622 Oryza sat
27	1.2	256	11	GI2716	GI2716
28	1.2	450	8	AF213398	AF213398 Ovis arie
29	1.2	897	6	AY536855	AY536855 Arabidops
30	1.2	897	6	AX546183	AX546183 Sequence
31	1.2	897	6	AX546184	AX546184 Sequence
32	1.2	897	6	AX546187	AX546187 Sequence
33	1.2	1185	8	AY224526	AY224526 Oryza sat
34	1.2	1281	6	AX546185	AX546185 Sequence
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37	1.2	3142	8	AY091180	AY091180 Human (pr-
38	1.2	3407	8	AY064019	AY064019 Arabidops
39	1.2	3677	9	HSMB08933	HSMB08933
40	1.2	4406	4	AY543631	AY543631 Canis fam
41	1.2	4419	4	AB118945	AB118945 Canis fam
42	1.2	4443	6	CQ727681	CQ727681 Sequence
43	1.2	4586	9	HSMBTPO	HSMBTPO
44	1.2	4620	6	CQ776403	CQ776403 Sequence
45	1.2	4620	6	AX546174	AX546174 Sequence
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48	1.2	4626	11	GI8239	GI8239
49	1.2	4823	4	AB112434	AB112434 Bos tauru
50	1.2	32173	9	AC004416	AC004416 Homo sapi
51	1.2	70311	23	AC002390	AC002390 Human DNA
52	1.2	73840	8	AB007644	AB007644 Arabidops
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54	1.2	116671	9	AC087264	AC087264 Pan trogl
55	1.2	121659	8	AC137001	AC137001 Oryza sat
56	1.2	137416	2	AC147842	AC147842 Ovis arie
57	1.2	141415	9	AC087214	AC087214 Papio anu
58	1.2	150635	4	AC130186	AC130186 Ateles
59	1.2	154207	2	AC149432	AC149432 Muntiacus
60	1.2	171944	2	AC138712	AC138712 Cercopit
61	1.2	174875	2	AC024682	AC024682 Homo sapi
62	1.2	176448	4	AC129886	AC129886 Ateles
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64	1.2	187829	2	AC139624	AC139624 Pongo pyg
65	1.2	197836	4	AC090032	AC090032 Canis fam
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68	1.2	208707	2	AC084729	AC084729 Papio anu
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71	1.1	71774	8	NCB9X17	NCB9X17 Neurospor
72	1.1	127576	5	OSJN00296	OSJN00296 Dancio rer
73	1.1	141099	8	OSJN00296	OSJN00296 Oryza sat
74	1.1	141491	8	OSJN00296	OSJN00296 Medicago
75	1.1	152676	8	OSJN00296	OSJN00296 Oryza sat
76	1.1	152676	8	OSJN00296	OSJN00296 Oryza sat
77	1.1	193421	9	AC107294	AC107294 Homo sapi
78	1.1	563	8	AY072046	AY072046 Trilicium
79	1.1	861	8	AF016274	AF016274 Arabidops
80	1.1	1250	6	BT012797	BT012797 Lycopersi
81	1.1	1250	6	BT012797	BT012797 Lycopersi
82	1.1	1639	8	TOBPSK	TOBPSK
83	1.1	1857	8	AY274811	AY274811 Homo sapi
84	1.1	1949	6	AX055443	AX055443 Sequence
85	1.1	2046	6	AX055443	AX055443 Sequence
86	1.1	2050	9	AY274811	AY274811 Homo sapi
87	1.1	2196	6	AX088879	AX088879 Sequence
88	1.1	2196	6	AX088879	AX088879 Sequence
89	1.1	2231	6	AX088878	AX088878 Sequence
90	1.1	2231	6	AX088878	AX088878 Sequence
91	1.1	2313	6	AX825708	AX825708 Sequence
92	1.1	2313	6	AX120541	AX120541 Oryza sat
93	1.1	2313	6	U00889	U00889 Hansenula p

C 93	21	1.1	2817	9	AK131385	AK131385 Homo sapi	166	21	1.1	240340	2	AC095354	AC095354 Rattus no
C 94	21	1.1	2837	8	AY059769	AY059769 Arabidops	167	21	1.1	242559	2	AC098256	AC098256 Rattus no
C 95	21	1.1	2891	6	AX105698	AX105698 Sequence	C 168	21	1.1	243005	2	AC134740	AC134740 Rattus no
C 96	21	1.1	3120	8	AF199021	AF199021 Chlamydom	169	21	1.1	245422	2	AC106225	AC106225 Rattus no
C 97	21	1.1	3764	9	HSMB02129	HSMB02129 Homo sapi	C 170	21	1.1	255952	2	AC106250	AC106250 Rattus no
C 98	21	1.1	3842	6	CQ841723	CQ841723 Sequence	C 171	21	1.1	262581	2	AC116220	AC116220 Rattus no
C 99	21	1.1	4237	9	AK124775	AK124775 Homo sapi	C 172	21	1.1	266049	2	AC103504	AC103504 Rattus no
C 100	21	1.1	5970	5	HSMB06302	HSMB06302 Homo sapi	C 173	21	1.1	274964	2	AC130982	AC130982 Rattus no
C 101	21	1.1	5970	5	AJ621356	AJ621356 Tetradodon	C 174	21	1.1	287501	2	AC098561	AC098561 Rattus no
C 102	21	1.1	7305	8	PTGWIN62B	PTGWIN62B Homo sapi	C 175	21	1.1	340493	10	EX883044	EX883044 Rattus no
C 103	21	1.1	10528	1	AE008644	AE008644 Rickettsi	C 176	21	1.1	349938	6	AX647882	AX647882 Sequence
C 104	21	1.1	15514	1	RRI293314	RRI293314 Rickettsi	C 177	20	1.0	150	8	CR378280	CR378280 pinus pin
C 105	21	1.1	17871	6	AX059525	AX059525 Sequence	C 178	20	1.0	213	6	CQ466837	CQ466837 Sequence
C 106	21	1.1	27960	6	AX059506	AX059506 Sequence	C 179	20	1.0	290	8	AY225995	AY225995 Sequence
C 107	21	1.1	40740	8	AC0077349	AC0077349 Homo sapi	C 180	20	1.0	334	3	AY380130	AY380130 Oreina el
C 108	21	1.1	80472	8	AC0077945	AC0077945 Genomica	C 181	20	1.0	339	11	BV0909332	BV0909332 Drosophila
C 109	21	1.1	82010	8	AB023042	AB023042 Arabidops	C 182	20	1.0	478	3	AY012605	AY012605 Drosophila
C 110	21	1.1	82532	8	AC006219	AC006219 Arabidops	C 183	20	1.0	500	9	AY520144	AY520144 Homo sapi
C 111	21	1.1	86455	2	AL137076	AL137076 Human DNA	C 184	20	1.0	500	9	AY520144	AY520144 Homo sapi
C 112	21	1.1	89259	9	AL137076	AL137076 Human DNA	C 185	20	1.0	506	8	CR377590	CR377590 pinus pin
C 113	21	1.1	90859	8	AC005561	AC005561 Arabidops	C 186	20	1.0	506	9	AY520143	AY520143 Homo sapi
C 114	21	1.1	99923	8	FS08	FS08 Arabidops	C 187	20	1.0	510	9	AY520143	AY520143 Homo sapi
C 115	21	1.1	108277	8	AP006108	AP006108 Locust cor	C 188	20	1.0	586	11	G88001	G88001 Sequence
C 116	21	1.1	110000	2	AC115142	AC115142 Rattus no	C 189	20	1.0	601	11	BV191997	BV191997 sqmml7295
C 117	21	1.1	110000	2	AC132992	AC132992 Rattus no	C 190	20	1.0	609	6	AR374755	AR374755 Sequence
C 118	21	1.1	1110000	8	CR382131	CR382131 Rattus no	C 191	20	1.0	657	6	AX765884	AX765884 Sequence
C 119	21	1.1	111780	8	AC146237	AC146237 Medicago	C 192	20	1.0	680	8	TOBCELPD	TOBCELPD Sequence
C 120	21	1.1	116780	8	AC146237	AC146237 Medicago	C 193	20	1.0	687	8	AK066856	AK066856 Elus mottle
C 121	21	1.1	131142	9	AP003156	AP003156 Homo sapi	C 194	20	1.0	690	14	EMT85402	EMT85402 Hydrangea
C 122	21	1.1	133410	5	BX470202	BX470202 Zebrafish	C 195	20	1.0	722	8	AK062598	AK062598 Rattus sat
C 123	21	1.1	133410	5	AC147001	AC147001 Medicago	C 196	20	1.0	773	11	BV026331	BV026331 Rattus sat
C 124	21	1.1	138181	8	AC005171	AC005171 Arabidops	C 197	20	1.0	786	8	AK105700	AK105700 Gorilla g
C 125	21	1.1	142937	2	AC139916	AC139916 Rattus no	C 198	20	1.0	896	9	AY520139	AY520139 Gorilla g
C 126	21	1.1	146742	2	AC069585	AC069585 Homo sapi	C 199	20	1.0	896	9	AY520140	AY520140 Gorilla g
C 127	21	1.1	149089	8	AP003991	AP003991 Oryza sat	C 200	20	1.0	922	5	AP506202	AP506202 Danio rer
C 128	21	1.1	151265	2	AC134756	AC134756 Rattus no	C 201	20	1.0	1002	6	AK059665	AK059665 Oryza sat
C 129	21	1.1	156678	2	AC149449	AC149449 Papio anu	C 202	20	1.0	1069	8	AK099480	AK099480 Arabidops
C 130	21	1.1	157583	5	BX571951	BX571951 Zebrafish	C 203	20	1.0	1153	8	AK118297	AK118297 Arabidops
C 131	21	1.1	164781	9	AC092440	AC092440 Homo sapi	C 204	20	1.0	1212	6	AX655977	AX655977 Sequence
C 132	21	1.1	166462	9	AC135074	AC135074 Homo sapi	C 205	20	1.0	1236	6	CR352526	CR352526 Gallus ga
C 133	21	1.1	171175	9	AC096674	AC096674 Homo sapi	C 206	20	1.0	1241	5	AF134305	AF134305 Homo sapi
C 134	21	1.1	176747	2	AC148954	AC148954 Otollemur	C 207	20	1.0	1368	9	CQ724305	CQ724305 Homo sapi
C 135	21	1.1	177434	2	AC116036	AC116036 Homo sapi	C 208	20	1.0	1509	6	AB026543	AB026543 Homo sapi
C 136	21	1.1	178119	9	AC027188	AC027188 Homo sapi	C 209	20	1.0	1540	10	AF420251	AF420251 Mus muscu
C 137	21	1.1	185244	2	AC087123	AC087123 Mus muscu	C 210	20	1.0	1701	6	BC077571	BC077571 Xenopus l
C 138	21	1.1	187746	2	AC120280	AC120280 Rattus no	C 211	20	1.0	1772	5	VPHEROPH	VPHEROPH Homo sapien
C 139	21	1.1	194431	2	AC142140	AC142140 Rattus no	C 212	20	1.0	1800	8	AT00688314	AT00688314 Rattus no
C 140	21	1.1	194866	2	AC125537	AC125537 Mus muscu	C 213	20	1.0	1830	9	AX088882	AX088882 Sequence
C 141	21	1.1	195987	10	AC135961	AC135961 Mus muscu	C 214	20	1.0	1849	5	AX825712	AX825712 Sequence
C 142	21	1.1	197411	10	AL603745	AL603745 Mouse DNA	C 215	20	1.0	1902	6	AX088881	AX088881 Sequence
C 143	21	1.1	198392	10	AL603745	AL603745 Mouse DNA	C 216	20	1.0	1939	6	AX825711	AX825711 Sequence
C 144	21	1.1	200635	2	AC111613	AC111613 Rattus no	C 217	20	1.0	1939	6	AX825710	AX825710 Sequence
C 145	21	1.1	201078	2	AC122220	AC122220 Mus muscu	C 218	20	1.0	1985	8	AB078412	AB078412 Ciona sav
C 146	21	1.1	202612	2	AC148952	AC148952 Otollemur	C 219	20	1.0	2042	5	BC041466	BC041466 Danio rer
C 147	21	1.1	206506	2	AC025585	AC025585 Mus muscu	C 220	20	1.0	2056	5	AK105266	AK105266 Oryza sat
C 148	21	1.1	206573	2	AC130594	AC130594 Rattus no	C 221	20	1.0	2064	5	BC067334	BC067334 Danio rer
C 149	21	1.1	206973	2	AC130867	AC130867 Rattus no	C 222	20	1.0	2064	5	BC067334	BC067334 Danio rer
C 150	21	1.1	208694	2	AC006295	AC006295 Homo sapi	C 223	20	1.0	2064	5	BC067334	BC067334 Danio rer
C 151	21	1.1	210000	2	AL662922	AL662922 Mouse DNA	C 224	20	1.0	2064	5	BC067334	BC067334 Danio rer
C 152	21	1.1	215916	10	AC126569	AC126569 Rattus no	C 225	20	1.0	2064	5	BC067334	BC067334 Danio rer
C 153	21	1.1	217622	2	AC025047	AC025047 Mus muscu	C 226	20	1.0	2064	5	BC067334	BC067334 Danio rer
C 154	21	1.1	220713	10	AC097412	AC097412 Rattus no	C 227	20	1.0	2064	5	BC067334	BC067334 Danio rer
C 155	21	1.1	221585	2	AC097412	AC097412 Rattus no	C 228	20	1.0	2064	5	BC067334	BC067334 Danio rer
C 156	21	1.1	222880	6	AX647883	AX647883 Sequence	C 229	20	1.0	2064	5	BC067334	BC067334 Danio rer
C 157	21	1.1	226519	2	AC095762	AC095762 Rattus no	C 230	20	1.0	2064	5	BC067334	BC067334 Danio rer
C 158	21	1.1	226601	10	AC122863	AC122863 Mus muscu	C 231	20	1.0	2064	5	BC067334	BC067334 Danio rer
C 159	21	1.1	227897	2	AC111962	AC111962 Rattus no	C 232	20	1.0	2064	5	BC067334	BC067334 Danio rer
C 160	21	1.1	228492	10	AC132058	AC132058 Rattus no	C 233	20	1.0	2064	5	BC067334	BC067334 Danio rer
C 161	21	1.1	232516	2	AC108828	AC108828 Mus muscu	C 234	20	1.0	2064	5	BC067334	BC067334 Danio rer
C 162	21	1.1	233405	2	AC126733	AC126733 Rattus no	C 235	20	1.0	2064	5	BC067334	BC067334 Danio rer
C 163	21	1.1	234746	10	CNS080CAS	AK044500 Mus muscu	C 236	20	1.0	2064	5	BC067334	BC067334 Danio rer
C 164	21	1.1	235343	2	AC121745	AC121745 Rattus no	C 237	20	1.0	2064	5	BC067334	BC067334 Danio rer
C 165	21	1.1	237997	2	AC093989	AC093989 Rattus no	C 238	20	1.0	2064	5	BC067334	BC067334 Danio rer



C 239	20	1.0	2755	10	MMU17698	U17698 Mus musculus	C 312	20	1.0	110000	2	BX324168_4	Continuation (5 of
C 240	20	1.0	2840	5	BC068922	BC068922 Xenopus 1	C 313	20	1.0	110000	8	CR380958_12	Continuation (13 o
C 241	20	1.0	2869	5	BD160752	BD160752 Method of	C 314	20	1.0	110000	8	CR382132_15	Continuation (16 o
C 242	20	1.0	2918	5	AF224315	AF224315 Gallus ga	C 315	20	1.0	110000	8	CR382132_22	Continuation (23 o
C 243	20	1.0	2962	10	BC079642	BC079642 Mus muscu	C 316	20	1.0	110000	8	AC145127_12	Continuation (13 o
C 244	20	1.0	3043	8	SPADASEN	X14488 S.pombe ade	C 317	20	1.0	111138	8	ATF1612	AL162459 Arabidops
C 245	20	1.0	3043	8	YSPADE6	M37264 S.pombe pho	C 318	20	1.0	117046	2	AC135600	AC135600 Oryza sat
C 246	20	1.0	3046	6	AX747634	AX747624 Sequence	C 319	20	1.0	118045	2	AC091665	AC091665 Oryza sat
C 247	20	1.0	3066	6	AK092602	AK092602 Homo sapi	C 320	20	1.0	118101	2	AC091665	AC091665 Oryza sat
C 248	20	1.0	3097	6	BD266932	BD266932 Compositi	C 321	20	1.0	118955	9	AC068274	AC068274 Homo sapi
C 249	20	1.0	3097	6	AR201531	AR201531 Sequence	C 322	20	1.0	119270	2	AY508219	AY508219 Medicago
C 250	20	1.0	3199	3	AB046873	AB046873 Halocynch	C 323	20	1.0	120476	2	AC130375	AC130375 Homo sapi
C 251	20	1.0	3234	5	BC073490	BC073490 Xenopus 1	C 324	20	1.0	120655	10	AL929140	AL929140 Mouse DNA
C 252	20	1.0	3271	10	BC004557	BC004557 Mus muscu	C 325	20	1.0	121309	9	AC026798	AC026798 Homo sapi
C 253	20	1.0	3431	14	SLU57047	U57047 Elm molitie	C 326	20	1.0	122390	2	AC135918	AC135918 Oryza sat
C 254	20	1.0	3475	3	AF303661	AF303661 Halocynch	C 327	20	1.0	122769	2	AC103371	AC103371 Mus muscu
C 255	20	1.0	3543	6	AX151655	AX151655 Sequence	C 328	20	1.0	123123	2	AC016610	AC016610 Homo sapi
C 256	20	1.0	3753	3	AY353563	AY353563 Anopheles	C 329	20	1.0	124191	9	AC005153	AC005153 Homo sapi
C 257	20	1.0	4005	3	HSW807100	BX640951 Homo sapi	C 330	20	1.0	124204	8	CNS08CCQ	AL954152 Oryza sat
C 258	20	1.0	4666	9	AK128724	AK128724 Homo sapi	C 331	20	1.0	124536	2	AC149107	AC149107 Papio anu
C 259	20	1.0	4698	10	AB033168	AB033168 Mus muscu	C 332	20	1.0	125153	4	AC087731	AL928778 Oryza sat
C 260	20	1.0	4705	9	AB020707	AB020707 Homo sapi	C 333	20	1.0	125661	9	HS1187M17	AC087731 Felis cat
C 261	20	1.0	4769	9	AF454702	AF454702 Homo sapi	C 334	20	1.0	125856	8	AP005200	AL121891 Human DNA
C 262	20	1.0	4823	9	BC050283	BC050283 Homo sapi	C 335	20	1.0	125909	8	OSJN00189	AP005200 Oryza sat
C 263	20	1.0	5720	6	AR374718	AR374718 Sequence	C 336	20	1.0	126447	9	AL592549	AL662985 Oryza sat
C 264	20	1.0	5868	6	AX026122	AX026122 Sequence	C 337	20	1.0	126447	8	OSJN00189	AL662985 Oryza sat
C 265	20	1.0	6034	8	AF205407	AF205407 Neurospor	C 338	20	1.0	129302	9	AL592549	AL592549 Human DNA
C 266	20	1.0	6316	6	AF179442	AF179442 Lycopersi	C 339	20	1.0	130740	8	AC133778	AC133778 Oryza sat
C 267	20	1.0	6916	6	AB026121	AB026121 Pseudomon	C 340	20	1.0	131414	8	AC144343	AC144343 Medicago
C 268	20	1.0	11608	1	ABE004757	ABE004757 Neurospor	C 341	20	1.0	131531	2	CNS09SC2	AC148088 Mus muscu
C 269	20	1.0	13701	1	AB124593	AB124593 Caenorhab	C 342	20	1.0	132854	8	OSJN00100	AL606654 Oryza sat
C 270	20	1.0	16975	2	AC019867	AC019867 Drosophil	C 343	20	1.0	133574	9	HS20N2	AL606654 Oryza sat
C 271	20	1.0	18653	2	AC019887	AC019887 Drosophil	C 344	20	1.0	134082	8	CNS08CAY	AL031370 Human DNA
C 272	20	1.0	32218	3	AF038615	AF038615 Caenorhab	C 345	20	1.0	134414	8	OSJN00200	AL844875 Oryza sat
C 273	20	1.0	36556	3	BX908402	BX908402 Human DNA	C 346	20	1.0	135940	8	AC116603	AL662999 Oryza sat
C 274	20	1.0	38822	3	CBRG01A11	AC084473 Caenorhab	C 347	20	1.0	137568	8	AC093178	AC116603 Oryza sat
C 275	20	1.0	41100	6	AX192230	AX192230 Sequence	C 348	20	1.0	138938	2	AC010111	AC093178 Oryza sat
C 276	20	1.0	42070	8	SPCC1222	AL035259 S.pombe c	C 349	20	1.0	139014	8	AF004233	AC010111 Drosophil
C 277	20	1.0	43709	8	BX649635	BX649635 Human DNA	C 350	20	1.0	139208	2	CR391998	AP004233 Oryza sat
C 278	20	1.0	49269	8	AC135499	AC135499 Oryza sat	C 351	20	1.0	139971	9	OSJN00294	CR391998 Oryza sat
C 279	20	1.0	61843	8	NC1586	AL153822 Neurospor	C 352	20	1.0	139971	8	AC007425	AL589843 Human DNA
C 280	20	1.0	65074	2	AC118706	AC118706 Mus muscu	C 353	20	1.0	140738	2	AC116517	AC007425 Homo sapi
C 281	20	1.0	65412	2	AC101325	AC101325 Mus muscu	C 354	20	1.0	142134	8	AP005632	AC116517 Homo sapi
C 282	20	1.0	68003	2	AC100827	AC100827 Mus muscu	C 355	20	1.0	142134	8	AP005632	AP005632 Oryza sat
C 283	20	1.0	68003	2	BX323853	BX323853 Homo sapi	C 356	20	1.0	142527	8	AL589843	AP003266 Oryza sat
C 284	20	1.0	69710	8	AP005969	AP005969 Oryza sat	C 357	20	1.0	143220	2	AC142159	AL589843 Human DNA
C 285	20	1.0	73305	8	NCB13A5	AL151345 Neurospor	C 358	20	1.0	143416	2	AC015470	AC142159 Homo sapi
C 286	20	1.0	73684	8	AC147804	AC147804 Homo sapi	C 359	20	1.0	144628	8	ATF4P12	AC015470 Homo sapi
C 287	20	1.0	73684	8	ABO22223	ABO22223 Arabidops	C 360	20	1.0	144738	2	AC112668	ATF4P12 Arabidops
C 288	20	1.0	77273	8	AC073555	AC073555 Arabidops	C 361	20	1.0	145100	8	AP005828	AC112668 Mus muscu
C 289	20	1.0	80561	8	AC128660	AC128660 Medicago	C 362	20	1.0	145107	8	AP004727	AP005828 Oryza sat
C 290	20	1.0	80716	2	AP005658	AP005658 Oryza sat	C 363	20	1.0	145526	8	AC079179	AP004727 Oryza sat
C 291	20	1.0	80896	8	AC006135	AC006135 Arabidops	C 364	20	1.0	146055	2	CNS08CBA	AC079179 Oryza sat
C 292	20	1.0	83356	8	AB013394	AB013394 Arabidops	C 365	20	1.0	147164	2	AP003834	AL731786 Oryza sat
C 293	20	1.0	85661	8	AC005882	AC005882 Arabidops	C 366	20	1.0	147198	8	AF466203	AP003834 Oryza sat
C 294	20	1.0	86394	8	AC145780	AC145780 Oryza sat	C 367	20	1.0	147344	8	AC091532	AF466203 Zea mays
C 295	20	1.0	88044	8	AC138543	AC138543 Magnapor	C 368	20	1.0	147486	10	AL670276	AC091532 Oryza sat
C 296	20	1.0	89464	2	AT15B16	AF104919 Arabidops	C 369	20	1.0	148179	9	AC093677	AL670276 Mouse DNA
C 297	20	1.0	90596	2	AC138708	AC138708 Homo sapi	C 370	20	1.0	148381	8	AP003253	AC093677 Homo sapi
C 298	20	1.0	91470	8	AP005769	AP005769 Homo sapi	C 371	20	1.0	148802	8	AP003207	AP003253 Oryza sat
C 299	20	1.0	91966	2	AC106439	AC106439 Arabidops	C 372	20	1.0	149181	8	OSJN00251	AP003207 Oryza sat
C 300	20	1.0	92861	8	AP006176	AP006176 Oryza sat	C 373	20	1.0	149318	2	AC091554	AL731602 Oryza sat
C 301	20	1.0	96205	8	HS28010	AC074219 Mus muscu	C 374	20	1.0	149414	8	BX957226	AC091554 Homo sapi
C 302	20	1.0	96700	8	AC103253	AC103253 Arabidops	C 375	20	1.0	149457	8	AP004193	BX957226 Datto rer
C 303	20	1.0	97700	8	AC148416	AC148416 Zea mays	C 376	20	1.0	149467	10	AC123235	AP004193 Oryza sat
C 304	20	1.0	101966	8	AP006059	AP006059 Oryza sat	C 377	20	1.0	149654	8	AC080019	AC123235 Homo sapi
C 305	20	1.0	106186	8	HS28010	AL118522 Human DNA	C 378	20	1.0	150128	8	AP005409	AC080019 Genomica s
C 306	20	1.0	106520	8	AP006059	AL118522 Human DNA	C 379	20	1.0	150552	8	AC148058	AP005409 Oryza sat
C 307	20	1.0	107109	8	HS28010	AL513122 Human DNA	C 380	20	1.0	151547	8	AP003312	AC148058 Calliobu
C 308	20	1.0	107120	2	AL513122	Continuation (5 of	C 381	20	1.0	152192	2	AC141346	AP003312 Oryza sat
C 309	20	1.0	108930	2	BX324168_4		C 382	20	1.0	152702	8	AP005162	AC141346 Rattus no
C 310	20	1.0	110000	2			C 383	20	1.0	152737	8	AC092931	AC005162 Oryza sat
C 311	20	1.0	110000	2			C 384	20	1.0	153939	2	AC110906	AC092931 Homo sapi

385	20	1.0	154137	8	AP003215	AP003215 Oryza sat	C 458	20	1.0	183467	2	AC133154	AC133154 Mus muscu
386	20	1.0	154494	2	AP005070	AP005070 Oryza sat	459	20	1.0	183917	2	AC093795	AC093795 Homo sapi
C 387	20	1.0	156757	2	AC144587	AC144587 Homo sapi	460	20	1.0	185048	9	AC093631	AC093631 Mus muscu
C 388	20	1.0	157237	8	AY542311	AY542311 Sorghum D	461	20	1.0	185320	8	AP006101	AP006101 Lotus cor
C 389	20	1.0	157539	8	AC136998	AC136998 Oryza sat	C 462	20	1.0	186330	8	AP005689	AP005689 Oryza sat
C 390	20	1.0	158430	2	AC012431	AC012431 Homo sapi	463	20	1.0	186719	2	AC147574	AC147574 Homo sapi
C 391	20	1.0	158493	8	AP003856	AP003856 Oryza sat	464	20	1.0	187471	8	AP004232	AP004232 Oryza sat
C 392	20	1.0	158693	9	AP005908	AP005908 Homo sapi	465	20	1.0	187605	2	AC141810	AC141810 Apis mell
C 393	20	1.0	159216	8	AP005870	AP005870 Oryza sat	466	20	1.0	187927	2	AC147924	AC147924 Xenopus t
C 394	20	1.0	159382	8	AC116601	AC116601 Oryza sat	467	20	1.0	188520	2	AC109298	AC109298 Mus muscu
C 395	20	1.0	159525	8	AC093493	AC093493 Oryza sat	468	20	1.0	189705	10	AC131088	AC131088 Mus muscu
C 396	20	1.0	159636	8	AC090485	AC090485 Genomimic S	469	20	1.0	189917	2	AC120606	AC120606 Rattus no
C 397	20	1.0	160895	2	AC142670	AC142670 Macaca mu	470	20	1.0	190679	2	AC147747	AC147747 Homo sapi
C 398	20	1.0	162568	8	AC136149	AC136149 Oryza sat	471	20	1.0	190680	9	AC147575	AC147575 Homo sapi
C 399	20	1.0	162797	2	AC023219	AC023219 Homo sapi	C 472	20	1.0	191918	2	AC026484	AC026484 Homo sapi
C 400	20	1.0	163115	9	AC105902	AC105902 Homo sapi	C 473	20	1.0	193168	2	AP001194	AP001194 Homo sapi
C 401	20	1.0	163130	8	AC117265	AC117265 Oryza sat	C 474	20	1.0	193625	2	AP001194	AP001194 Homo sapi
C 402	20	1.0	163597	8	AP003333	AP003333 Oryza sat	475	20	1.0	193626	2	CR391971	CR391971 Dantio rer
C 403	20	1.0	163996	8	AP003333	AP003333 Oryza sat	476	20	1.0	194068	2	AC115327	AC115327 Rattus no
C 404	20	1.0	164236	8	AC133339	AC133339 Oryza sat	477	20	1.0	194476	2	AC147745	AC147745 Homo sapi
C 405	20	1.0	164850	8	AC135498	AC135498 Oryza sat	478	20	1.0	194599	2	AC073668	AC073668 Mus muscu
C 406	20	1.0	165090	2	AC141921	AC141921 Rattus no	C 479	20	1.0	195432	2	AC130403	AC130403 Homo sapi
C 407	20	1.0	165094	8	OSJN00154	AL662951 Oryza sat	C 480	20	1.0	196124	2	AC141387	AC141387 Rattus no
C 408	20	1.0	165443	2	AC148167	AC148167 Zea mays	481	20	1.0	196432	2	AC147601	AC147601 Homo sapi
C 409	20	1.0	165957	8	AP006523	AP006523 Oryza sat	482	20	1.0	196938	10	AL672218	AL672218 Mouse DNA
C 410	20	1.0	166233	2	AC079939	AC079939 Mus muscu	483	20	1.0	197238	2	AC124534	AC124534 Mus muscu
C 411	20	1.0	166233	2	AC079939	AC079939 Oryza sat	484	20	1.0	197411	2	AC107734	AC107734 Homo sapi
C 412	20	1.0	166320	9	AC019349	AC123273 Rattus no	C 485	20	1.0	198356	9	AC081035	AC081035 Mus muscu
C 413	20	1.0	166508	8	OSJN08CA1	AL831805 Oryza sat	C 486	20	1.0	198356	2	AC087138	AC087138 Homo sapi
C 414	20	1.0	166747	8	OSJN00208	AL831805 Oryza sat	487	20	1.0	198578	8	ATCHR1V4	ATCHR1V4 Arabidops
C 415	20	1.0	167357	2	AC140785	AL663005 Oryza sat	C 488	20	1.0	198697	2	AC138591	AC138591 Mus muscu
C 416	20	1.0	167834	2	AC148164	AC140785 Mus muscu	C 489	20	1.0	199261	2	AC101924	AC101924 Oryza sat
C 417	20	1.0	168011	8	AL158150	AC148164 Zea mays	C 490	20	1.0	200361	2	OSJN00284	OSJN00284 Homo sapi
C 418	20	1.0	168252	8	AP003021	AL158150 Human DNA	C 491	20	1.0	201427	2	AC127843	AC127843 Rattus no
C 419	20	1.0	168430	8	AC126221	AP003021 Oryza sat	C 492	20	1.0	201466	2	AC147573	AC147573 Homo sapi
C 420	20	1.0	168641	10	AC115911	AC126221 Oryza sat	C 493	20	1.0	204038	2	AC133520	AC133520 Mus muscu
C 421	20	1.0	169138	3	AC010571	AC115911 Mus muscu	C 494	20	1.0	204627	2	EX510655	EX510655 Homo sapi
C 422	20	1.0	169270	8	AC083943	AC010571 Drosophill	C 495	20	1.0	206442	2	AL158978	AL158978 Mus muscu
C 423	20	1.0	169506	8	AP005464	AC083943 Genomimic s	496	20	1.0	206514	2	AC100728	AC100728 Mus muscu
C 424	20	1.0	169662	8	CNS07YFX	AP005464 Oryza sat	C 497	20	1.0	206695	2	AC091466	AC091466 Oryctolag
C 425	20	1.0	169693	2	AC118440	AL713952 Oryza sat	498	20	1.0	206755	4	AC006558	AC006558 Homo sapi
C 426	20	1.0	170064	8	AP003771	AC118440 Rattus no	499	20	1.0	207392	2	AC006558	AC006558 Homo sapi
C 427	20	1.0	170228	8	AP005829	AP003771 Oryza sat	500	20	1.0	207555	2	AC118714	AC118714 Mus muscu
C 428	20	1.0	170894	2	AC136648	AP005829 Oryza sat	501	20	1.0	208462	9	AC130686	AC130686 Homo sapi
C 429	20	1.0	172116	2	AC009472	AC136648 Rattus no	502	20	1.0	209206	2	AC105971	AC105971 Homo sapi
C 430	20	1.0	173204	2	AC127524	AC009472 Homo sapi	503	20	1.0	209336	2	AY542798	AY542798 Zea mays
C 431	20	1.0	173374	8	AC146340	AC127524 Genomimic s	504	20	1.0	209354	2	AC068752	AC068752 Homo sapi
C 432	20	1.0	173977	8	AC010170	AC146340 Homo sapi	505	20	1.0	210476	10	AC087166	AC087166 Mus muscu
C 433	20	1.0	174011	8	AP006554	AC010170 Homo sapi	506	20	1.0	212011	2	AC136410	AC136410 Mus muscu
C 434	20	1.0	174498	2	AC147746	AP006554 Oryza sat	507	20	1.0	21686	2	AC119896	AC119896 Mus muscu
C 435	20	1.0	174836	2	AC122766	AC147746 Homo sapi	508	20	1.0	215123	10	AC113542	AC113542 Mus muscu
C 436	20	1.0	174914	9	AC068874	AC122766 Mus muscu	509	20	1.0	215497	4	AC141564	AC141564 Mus muscu
C 437	20	1.0	175313	2	BX005160	AC068874 Homo sapi	C 510	20	1.0	215926	10	AC098719	AC098719 Mus muscu
C 438	20	1.0	176977	2	AC105784	BX005160 Dantio rer	C 511	20	1.0	216345	2	AC131805	AC131805 Rattus no
C 439	20	1.0	177191	2	AC145146	AC105784 Rattus no	C 512	20	1.0	216345	2	AC131805	AC131805 Rattus no
C 440	20	1.0	177268	2	AC145286	AC145146 Homo sapi	C 513	20	1.0	216472	2	AC149588	AC149588 Homo sapi
C 441	20	1.0	177827	2	AC123743	AC145286 Homo sapi	C 514	20	1.0	217766	10	AC087558	AC087558 Mus muscu
C 442	20	1.0	177899	10	AC123042	AC123743 Mus muscu	C 515	20	1.0	218712	2	AC103917	AC103917 Homo sapi
C 443	20	1.0	178320	8	AY360391	AC123042 Mus muscu	C 516	20	1.0	219345	9	AC116238	AC116238 Rattus no
C 444	20	1.0	178607	3	AC010068	AY360391 Oryza sat	C 517	20	1.0	219602	2	AC006952	AC006952 Homo sapi
C 445	20	1.0	178789	2	AC124108	AC010068 Drosophill	C 518	20	1.0	219626	10	AC098719	AC098719 Mus muscu
C 446	20	1.0	179374	10	AC009357	AC124108 Mus muscu	C 519	20	1.0	220460	2	AC122740	AC122740 Mus muscu
C 447	20	1.0	181098	9	AC0084216	AC140335 Mus muscu	C 520	20	1.0	222817	2	AC137185	AC137185 Rattus no
C 448	20	1.0	181098	9	AC0084216	AC009357 Drosophill	C 521	20	1.0	223183	2	AC131805	AC131805 Rattus no
C 449	20	1.0	181633	3	AC0088224	AC0084216 Homo sapi	C 522	20	1.0	223183	2	AC110952	AC110952 Rattus no
C 450	20	1.0	181974	2	BX936406	AC0088224 Drosophill	C 523	20	1.0	223632	2	AC122741	AC122741 Mus muscu
C 451	20	1.0	182079	2	OSJN00133	BX936406 Dantio rer	C 524	20	1.0	223632	2	AC106939	AC106939 Rattus no
C 452	20	1.0	182923	5	AL954767	AL662943 Oryza sat	C 525	20	1.0	223927	2	AC079441	AC079441 Mus muscu
C 453	20	1.0	183058	2	AL954767	AL662943 Oryza sat	C 526	20	1.0	224352	2	AC103271	AC103271 Rattus no
C 454	20	1.0	183137	2	CNS048130	AL954767 Zebrafish	C 527	20	1.0	224732	2	AC120221	AC120221 Rattus no
C 455	20	1.0	183353	10	CNS048130	AL954767 Zebrafish	C 528	20	1.0	224786	2	AC118501	AC118501 Rattus no
C 456	20	1.0	183385	9	CNS08CPO	AL954767 Mouse DNA	C 529	20	1.0	224846	10	AC125327	AC125327 Mus muscu
C 457	20	1.0	183459	8	AC142525	AL954767 Mouse DNA	C 530	20	1.0	225726	2	AC074328	AC074328 Mus muscu

531	20	1.0	226001	8	AF391808	Zea mays	604	19	1.0	201	11	BV207405	BV207405 sqm22340
532	20	1.0	226303	2	AC133489	Mus muscu	605	19	1.0	201	11	BV207408	BV207408 sqm22341
533	20	1.0	227691	2	AC110885	Mus muscu	606	19	1.0	211	5	CHKMET	D38404 Chicken mri
534	20	1.0	228931	2	AC131355	Rattus no	607	19	1.0	215	12	AR463529	AR463529 Synthetic
535	20	1.0	229256	2	AC128826	Rattus no	608	19	1.0	235	8	CR354473	CR354473 Pinus pin
536	20	1.0	230449	2	BX601648	Danio rer	609	19	1.0	243	8	CR377681	CR377681 Pinus pin
537	20	1.0	230672	10	AL772397	Mouse DNA	610	19	1.0	250	8	CR377447	CR377447 Pinus pin
538	20	1.0	231989	10	AL805897	Mouse DNA	611	19	1.0	295	11	BV088106	BV088106 D4Mon47 R
539	20	1.0	233933	2	AC128903	Rattus no	612	19	1.0	296	6	AX363361	AX363361 Sequence
540	20	1.0	234580	2	AC130855	Rattus no	613	19	1.0	302	3	AY186678	AY186678 Cancer ma
541	20	1.0	234675	2	AC097407	Rattus no	614	19	1.0	333	6	AY80895	AY80895 Sequence 22
542	20	1.0	236096	2	AC094782	Rattus no	615	19	1.0	358	6	AR147989	AR147989 Sequence
543	20	1.0	237630	2	AC106665	Rattus no	616	19	1.0	358	6	AR219713	AR219713 Sequence
544	20	1.0	238372	2	AC096926	Rattus no	617	19	1.0	358	6	AR433187	AR433187 Sequence
545	20	1.0	241381	10	AC087063	Mus muscu	618	19	1.0	358	6	AX116831	AX116831 Sequence
546	20	1.0	241522	2	AC137599	Oryza sat	619	19	1.0	358	6	BD084364	BD084364 Compositi
547	20	1.0	241543	2	AC099472	Rattus no	620	19	1.0	437	6	AX886919	AX886919 Sequence
548	20	1.0	241887	2	AC094044	Rattus no	621	19	1.0	437	6	BD026529	BD026529 Sequence
549	20	1.0	245548	2	AC112899	Rattus no	622	19	1.0	437	6	BT006546	BT006546 Arabidops
550	20	1.0	246577	2	AC136124	Rattus no	623	19	1.0	462	8	C0069746	C0069746 Sequence
551	20	1.0	246805	2	AC098750	Rattus no	624	19	1.0	462	8	C0069746	C0069746 Sequence
552	20	1.0	247248	2	AC106695	Rattus no	625	19	1.0	463	6	CQ069699	CQ069699 Sequence
553	20	1.0	247575	2	AC133047	Rattus no	626	19	1.0	463	6	CQ135808	CQ135808 Sequence
554	20	1.0	247588	10	AC114512	Rattus no	627	19	1.0	463	6	CQ174113	CQ174113 Sequence
555	20	1.0	248059	2	AC137556	Rattus no	628	19	1.0	463	6	CQ219104	CQ219104 Sequence
556	20	1.0	248529	2	AC097592	Rattus no	629	19	1.0	463	6	CQ257654	CQ257654 Sequence
557	20	1.0	249274	2	AC123329	Rattus no	630	19	1.0	463	6	CQ294911	CQ294911 Sequence
558	20	1.0	249632	2	AC096927	Rattus no	631	19	1.0	463	6	CQ331560	CQ331560 Sequence
559	20	1.0	249661	2	AC130081	Rattus no	632	19	1.0	479	11	AU026793	AU026793 Rattus no
560	20	1.0	251533	2	AC125364	Rattus no	633	19	1.0	524	8	AB108371	AB108371 Phleum pr
561	20	1.0	251710	2	AC117065	Rattus no	634	19	1.0	524	8	CR354486	CR354486 Pinus pin
562	20	1.0	251773	2	AC079129	Mus muscu	635	19	1.0	531	6	C0078970	C0078970 Sequence
563	20	1.0	252187	2	AC125998	Rattus no	636	19	1.0	531	6	CQ110189	CQ110189 Sequence
564	20	1.0	252889	2	AC120743	Rattus no	637	19	1.0	531	6	CQ148898	CQ148898 Sequence
565	20	1.0	253184	2	AC137219	Rattus no	638	19	1.0	531	6	CQ184031	CQ184031 Sequence
566	20	1.0	253328	2	AC130341	Homo sapi	639	19	1.0	531	6	CQ232171	CQ232171 Sequence
567	20	1.0	255446	2	AC095420	Rattus no	640	19	1.0	531	6	CQ270276	CQ270276 Sequence
568	20	1.0	255818	2	AC145871	Fan trogl	641	19	1.0	531	6	CQ307485	CQ307485 Sequence
569	20	1.0	256476	10	AC126940	Mus muscu	642	19	1.0	531	6	CQ344355	CQ344355 Sequence
570	20	1.0	259158	2	AC099470	Rattus no	643	19	1.0	547	8	CR377638	CR377638 Pinus pin
571	20	1.0	260517	2	AC111318	Rattus no	644	19	1.0	554	11	G94971	G94971 S208P6791.F
572	20	1.0	260517	2	AC097621	Rattus no	645	19	1.0	566	11	G63087	G63087 SHGC-140687
573	20	1.0	261056	2	AC119075	Rattus no	646	19	1.0	585	8	AAARNARP1	X84216 A.alternata
574	20	1.0	261056	2	AC119075	Rattus no	647	19	1.0	585	8	AAARNARP1	G88235 S208P6768RC
575	20	1.0	267749	2	AC131472	Rattus no	648	19	1.0	595	11	G88235	AY099799 Arabidops
576	20	1.0	268151	2	AC111391	Rattus no	649	19	1.0	609	8	AX653925	AX653925 Sequence
577	20	1.0	270068	2	AC113313	Rattus no	650	19	1.0	615	6	CR377924	CR377924 Pinus pin
578	20	1.0	270962	2	AC149067	Mus muscu	651	19	1.0	615	6	AY085879	AY085879 Arabidops
579	20	1.0	271101	2	AC132376	Mus muscu	652	19	1.0	636	8	AK121661	AK121661 Oryza sat
580	20	1.0	274695	2	AC127582	Mus muscu	653	19	1.0	693	8	AY057736	AY057736 Arabidops
581	20	1.0	278572	10	AF287263	Mus muscu	654	19	1.0	697	10	BC033478	BC033478 Mus muscu
582	20	1.0	283050	1	BX294150	Mus muscu	655	19	1.0	704	8	AF053076	AF053076
583	20	1.0	283274	2	AC055759	AC055759 Homo sapi	656	19	1.0	706	11	BV053884	BV053884 S212P6371
584	20	1.0	292967	14	AF369029	AF369029 White spo	657	19	1.0	813	5	BC073447	BC073447 Xenopus 1
585	20	1.0	294272	2	AE003595	AE003595 Drosophill	658	19	1.0	833	6	BD020352	BD020352 Novel gen
586	20	1.0	299325	1	AP005039	AP005039 Streptomy	659	19	1.0	833	6	BD100290	BD100290 Novel gen
587	20	1.0	300023	8	AE017051	AE017051 Oryza sat	660	19	1.0	833	6	AK059288	AK059288 Oryza sat
588	20	1.0	300023	8	AE017051	AE017051 Oryza sat	661	19	1.0	842	8	AY220736	AY220736 Hordeum v
589	20	1.0	300029	8	AE017056	AE017056 Oryza sat	662	19	1.0	865	10	BC002184	BC002184 Mus muscu
590	20	1.0	300800	1	SC0939112	SC0939112 Streptomy	663	19	1.0	872	10	BC069888	BC069888 Mus muscu
591	20	1.0	300964	8	AE016890	AE016890 Eremothec	664	19	1.0	906	8	D86854	D86854 Catharanthu
592	20	1.0	302228	8	AE017070	AE017070 Oryza sat	665	19	1.0	917	8	AB104612	AB104612 Daucus ca
593	20	1.0	302228	8	AE017070	AE017070 Oryza sat	666	19	1.0	960	10	AK109434	AK109434 Oryza sat
594	20	1.0	304297	8	AE017088	AE017088 Oryza sat	667	19	1.0	960	10	MMP5212	MMP5212 Mus muscu
595	20	1.0	305107	8	AX151396	AX151396 Sequence	668	19	1.0	975	8	AF510219	AF510219 Saccharom
596	20	1.0	305107	14	AF333093	AF333093 White spo	669	19	1.0	975	8	AF510220	AF510220 Saccharom
597	20	1.0	305166	3	AE003601	AE003601 Drosophill	670	19	1.0	985	6	AX111225	AX111225 Sequence
598	20	1.0	307287	14	AF440570	AF440570 Shrimp wh	671	19	1.0	1001	8	AK060891	AK060891 Oryza sat
599	20	1.0	318505	2	AC123174	AC123174 Rattus no	672	19	1.0	1041	8	AF510221	AF510221 Saccharom
600	20	1.0	324367	2	AE017091	AE017091 Rattus no	673	19	1.0	1044	8	AK105895	AK105895 Oryza sat
601	20	1.0	326363	2	AC139857	Mus muscu	674	19	1.0	1046	8	AK069514	AK069514 Oryza sat
602	19	1.0	189	6	AX700758	AX700758 Sequence	675	19	1.0	1053	5	BC073408	BC073408 Xenopus 1
603	19	1.0	201	11	BV201540	BV201540 sqm20684	676	19	1.0				

677	19	1.0	1107	8	AF510222	AF510222	Saccharom	750	19	1.0	2501	6	CQ778532	CQ778532	Sequence
678	19	1.0	1120	9	HSU55963	U15963	Human	751	19	1.0	2513	8	AK101520	AK101520	Oryza sat
679	19	1.0	1128	8	AY045684	AY045684	Arabidops	752	19	1.0	2601	8	BD180282	BD180282	Higly th
680	19	1.0	1128	8	AF510223	AF510223	Saccharom	753	19	1.0	2603	6	AX714069	AX714069	Sequence
C 681	19	1.0	1130	8	AK121889	AK121889	Oryza sat	C 754	19	1.0	2603	9	AK056137	AK056137	Homo sapi
682	19	1.0	1140	5	AF145944	AF145944	Barbus lu	C 755	19	1.0	2653	10	BC031135	BC031135	Mus muscu
683	19	1.0	1140	5	AF145947	AF145947	Barbus ca	756	19	1.0	2746	6	AX883125	AX883125	Sequence
684	19	1.0	1140	5	AF180831	AF180831	Barbus ch	757	19	1.0	2746	6	BD160141	BD160141	Primer fo
685	19	1.0	1140	5	AF180852	AF180852	Barbus ha	758	19	1.0	2746	8	AK023671	AK023671	Homo sapi
686	19	1.0	1140	5	AF180855	AF180855	Barbus hu	C 759	19	1.0	2767	8	AY485636	AY485636	Uetillago
687	19	1.0	1140	5	AF180864	AF180864	Barbus vu	C 760	19	1.0	2795	10	BC016131	BC016131	Mus muscu
688	19	1.0	1140	5	AF180866	AF180866	Varicorhi	C 761	19	1.0	2795	8	AK119325	AK119325	Oryza sat
689	19	1.0	1140	5	AF180876	AF180876	Barbus ae	C 762	19	1.0	3064	8	AY035076	AY035076	Arabidops
690	19	1.0	1140	5	AF180877	AF180877	Barbus po	763	19	1.0	3073	8	AK099582	AK099582	Oryza sat
691	19	1.0	1141	5	AF287431	AF287431	Barbus gr	764	19	1.0	3085	9	AK074251	AK074251	Homo sapi
692	19	1.0	1141	5	AF287448	AF287448	Barbus vu	C 765	19	1.0	3104	8	AK065680	AK065680	Oryza sat
693	19	1.0	1141	5	AF288486	AF288486	Barbus ca	C 766	19	1.0	3104	14	AB102675	AB102675	Rosellini
694	19	1.0	1142	5	AF201581	AF201581	Campylomo	C 767	19	1.0	3517	6	AX746577	AX746577	Sequence
C 695	19	1.0	1173	8	AF559047	AF559047	Oryza sat	C 768	19	1.0	3517	6	AK090691	AK090691	Homo sapi
696	19	1.0	1194	8	AF510224	AF510224	Saccharom	C 769	19	1.0	3621	6	AR300472	AR300472	Sequence
697	19	1.0	1238	8	BC040733	BC040733	Homo sapi	C 770	19	1.0	3621	6	AR428749	AR428749	Sequence
C 698	19	1.0	1243	8	AK065256	AK065256	Oryza sat	C 771	19	1.0	3621	6	AR442838	AR442838	Sequence
699	19	1.0	1260	8	AF510225	AF510225	Saccharom	C 772	19	1.0	3641	6	CQ716253	CQ716253	Sequence
700	19	1.0	1281	8	AF510226	AF510226	Saccharom	C 773	19	1.0	3641	6	HIMECTPH	HIMECTPH	Human prote
C 701	19	1.0	1307	8	AY088839	AY088839	Arabidops	C 774	19	1.0	3783	6	AR300471	AR300471	Sequence
702	19	1.0	1332	5	XLP40PK	X53962	Xenopus MO1	C 775	19	1.0	3783	6	AR442837	AR442837	Sequence
C 703	19	1.0	1336	10	BC079131	BC079131	Rattus no	C 776	19	1.0	3807	6	AR442837	AR442837	Sequence
704	19	1.0	1447	5	CR523638	CR523638	Gallus ga	C 777	19	1.0	3807	6	AR442837	AR442837	Sequence
705	19	1.0	1467	3	AF216742	AF216742	Typanoso	C 778	19	1.0	3831	6	CQ730760	CQ730760	Sequence
C 706	19	1.0	1528	8	NTA438265	NTA438265	Nicotiana	C 779	19	1.0	3879	6	CQ576588	CQ576588	Sequence
707	19	1.0	1531	8	BT006037	BT006037	Arabidops	C 780	19	1.0	4010	9	AK122932	AK122932	Homo sapi
C 708	19	1.0	1542	10	AY640307	AY640307	Mus muscu	C 781	19	1.0	4174	6	CQ611597	CQ611597	Sequence
C 709	19	1.0	1542	8	BT008878	BT008878	Arabidops	C 782	19	1.0	4174	6	CQ577748	CQ577748	Sequence
C 710	19	1.0	1572	8	AY093313	AY093313	Arabidops	C 783	19	1.0	4277	6	AX468106	AX468106	Sequence
711	19	1.0	1582	8	AK064240	AK064240	Oryza sat	C 784	19	1.0	4369	5	GGRNACMET	GGRNACMET	Sequence
C 712	19	1.0	1583	8	AB090881	AB090881	Aster tti	C 785	19	1.0	4456	3	BT010034	BT010034	Sequence
713	19	1.0	1650	8	AK103739	AK103739	Oryza sat	C 786	19	1.0	4456	3	CQ591494	CQ591494	Sequence
714	19	1.0	1659	8	AK128818	AK128818	Homo sapi	C 787	19	1.0	4461	6	CQ727154	CQ727154	Sequence
715	19	1.0	1704	6	AX652967	AX652967	Sequence	C 788	19	1.0	4515	6	CQ574682	CQ574682	Sequence
C 716	19	1.0	1716	8	AY062534	AY062534	Arabidops	C 789	19	1.0	4624	9	AF227905	AF227905	Homo sapi
C 717	19	1.0	1718	8	BC071687	BC071687	Homo sapi	C 790	19	1.0	4927	2	AK129214	AK129214	Mus muscu
C 718	19	1.0	1731	8	AF266870	AF266870	Aspergilli	C 791	19	1.0	4930	10	BT010212	BT010212	Drosophila
C 719	19	1.0	1743	8	AF094825	AF094825	Birassica	C 792	19	1.0	5007	3	BT010212	BT010212	Drosophila
C 720	19	1.0	1750	8	AK122010	AK122010	Oryza sat	C 793	19	1.0	5042	6	AX405692	AX405692	Sequence
C 721	19	1.0	1757	8	AY092962	AY092962	Arabidops	C 794	19	1.0	5053	6	AR211482	AR211482	Sequence
C 722	19	1.0	1790	10	BC057448	BC057448	Mus muscu	C 795	19	1.0	5053	6	AX085613	AX085613	Sequence
C 723	19	1.0	1796	10	BC026588	BC026588	Mus muscu	C 796	19	1.0	5053	10	AF200359	AF200359	Rattus no
C 724	19	1.0	1831	3	AK069193	AK069193	Rhynchopu	C 797	19	1.0	5242	10	BC049106	BC049106	Mus muscu
C 725	19	1.0	1927	3	AY122622	AY122622	Rhynchopu	C 798	19	1.0	5252	10	BC068283	BC068283	Mus muscu
726	19	1.0	1933	8	AK093415	AK093415	Homo sapi	C 799	19	1.0	5543	9	AB018345	AB018345	Sequence
727	19	1.0	1978	8	AK117505	AK117505	Arabidops	C 800	19	1.0	5580	10	BC068283	BC068283	Mus muscu
728	19	1.0	2000	6	AX655891	AX655891	Sequence	C 801	19	1.0	5597	6	AR300462	AR300462	Sequence
729	19	1.0	2011	9	AK128817	AK128817	Homo sapi	C 802	19	1.0	5597	6	AR428739	AR428739	Sequence
730	19	1.0	2013	8	BT005955	BT005955	Arabidops	C 803	19	1.0	5597	6	AR442828	AR442828	Sequence
731	19	1.0	2025	6	AX088885	AX088885	Sequence	C 804	19	1.0	6616	6	AX345377	AX345377	Sequence
732	19	1.0	2025	6	AX825715	AX825715	Sequence	C 805	19	1.0	6625	6	CQ599108	CQ599108	Sequence
C 733	19	1.0	2026	5	OMV427867	OMV427867	Oncorhync	C 806	19	1.0	6684	6	AX252004	AX252004	Sequence
734	19	1.0	2037	8	AK106734	AK106734	Oryza sat	C 807	19	1.0	6754	6	AX348777	AX348777	Sequence
735	19	1.0	2063	9	AK074376	AK074376	Homo sapi	C 808	19	1.0	6802	5	AY217453	AY217453	Human papil
736	19	1.0	2094	6	BC044310	BC044310	Homo sapi	C 809	19	1.0	6802	5	PEH11	PEH11	Sequence
737	19	1.0	2104	6	AX088884	AX088884	Sequence	C 810	19	1.0	9567	3	DMU25586	DMU25586	Sequence
738	19	1.0	2104	6	AX825714	AX825714	Mus muscu	C 811	19	1.0	9567	3	AX664484	AX664484	Sequence
C 739	19	1.0	2158	10	BC058764	BC058764	Mus muscu	C 812	19	1.0	12257	1	AB009793	AB009793	Pyrobacul
740	19	1.0	2158	5	BC067309	BC067309	Xenopus t	C 813	19	1.0	12499	2	AC017696	AC017696	Drosophila
741	19	1.0	2227	5	PEH1671V	PEH1671V	Human papil	C 814	19	1.0	12839	6	CQ584729	CQ584729	Sequence
C 742	19	1.0	2260	14	AK072690	AK072690	Oryza sat	C 815	19	1.0	13514	6	CQ576587	CQ576587	Sequence
743	19	1.0	2263	8	AK118488	AK118488	Arabidops	C 816	19	1.0	15579	6	CQ806572	CQ806572	Sequence
744	19	1.0	2320	8	BC023910	BC023910	Mus muscu	C 817	19	1.0	15579	6	CQ806572	CQ806572	Sequence
745	19	1.0	2381	10	AR392138	AR392138	Sequence	C 818	19	1.0	15579	6	AX795680	AX795680	Sequence
C 746	19	1.0	2421	6	BD082200	BD082200	Activity	C 819	19	1.0	15579	6	AX795680	AX795680	Sequence
C 747	19	1.0	2421	6	BD082200	BD082200	Activity	C 820	19	1.0	15579	6	AX795680	AX795680	Sequence
C 748	19	1.0	2487	6	AR392148	AR392148	Sequence	C 821	19	1.0	15579	6	AX822129	AX822129	Sequence
C 749	19	1.0	2487	10	AF068198	AF068198	Mus muscu	C 822	19	1.0	16579	6	AX822282	AX822282	Sequence

C 823	19	1.0	16579	6	AX825594	C 896	19	1.0	98942	8	F24U5	AC008075	Arabidops
C 824	19	1.0	16579	6	AX825601	897	19	1.0	98955	2	AC008886	AC008886	Homo sapi
C 825	19	1.0	16579	6	AX825769	898	19	1.0	99322	9	AC046184	AC046184	Homo sapi
C 826	19	1.0	16579	6	AX825922	899	19	1.0	99960	8	TRP20	AC018748	Homo sapi
C 827	19	1.0	16750	6	AX251068	C 900	19	1.0	102178	8	AP003803	AP003803	Oryza sat
C 828	19	1.0	16750	6	AX345423	C 901	19	1.0	104481	2	AP003844	AP003844	Oryza sat
C 829	19	1.0	18964	8	CRR242525	902	19	1.0	104485	9	AC069439	AC069439	Homo sapi
C 830	19	1.0	22022	8	AB025640	903	19	1.0	105787	9	AC113367	AC113367	Homo sapi
C 831	19	1.0	23889	3	CER02A10	904	19	1.0	106942	8	AP003835	AP003835	Homo sapi
C 832	19	1.0	25337	2	AC014683	905	19	1.0	107480	9	AL596094	AL596094	Homo sapi
C 833	19	1.0	28078	2	CER21F12	C 906	19	1.0	107815	8	AP004157	AP004157	Oryza sat
C 834	19	1.0	29594	3	AC014129	C 907	19	1.0	107815	8	AC002482	AC002482	Human BAC
C 835	19	1.0	30480	3	CER2B3	C 908	19	1.0	108012	8	AL713868	AL713868	Human DNA
C 836	19	1.0	30615	2	AC18027	C 909	19	1.0	108058	8	AP000710	AP000710	Neurospor
C 837	19	1.0	30889	2	AC149350	C 910	19	1.0	108464	2	BX324141	BX324141	Homo sapi
C 838	19	1.0	32572	6	AX358994	C 911	19	1.0	109964	5	AP005677	AP005677	Oryza sat
C 839	19	1.0	32621	14	AF289262	C 912	19	1.0	109964	5	AC095760	AC095760	Rattus no
C 840	19	1.0	33369	3	AC148924	C 913	19	1.0	109964	2	AC095760	AC095760	Rattus no
C 841	19	1.0	33520	3	CER02E1	C 914	19	1.0	110000	2	AC095760	AC095760	Rattus no
C 842	19	1.0	33782	3	CERK09	C 915	19	1.0	110000	2	AC103465	AC103465	Continuation (4 of
C 843	19	1.0	34934	3	AC148914	C 916	19	1.0	110000	2	AC103465	AC103465	Continuation (4 of
C 844	19	1.0	35955	3	CERF3B7	C 917	19	1.0	110000	2	AC10829	AC10829	Continuation (2 of
C 845	19	1.0	37497	2	AC017356	C 918	19	1.0	110000	2	AC10829	AC10829	Continuation (2 of
C 846	19	1.0	39366	2	BS000569	C 919	19	1.0	110000	2	AC110950	AC110950	Continuation (2 of
C 847	19	1.0	39534	3	CERK643	C 920	19	1.0	110000	2	AC113742	AC113742	Continuation (2 of
C 848	19	1.0	43570	8	AB019231	C 921	19	1.0	110000	2	AC115429	AC115429	Continuation (2 of
C 849	19	1.0	43802	3	CERK07F5	C 922	19	1.0	110000	2	AC115429	AC115429	Continuation (2 of
C 850	19	1.0	44057	9	HSCN37F10	C 923	19	1.0	110000	2	AC128128	AC128128	Continuation (2 of
C 851	19	1.0	50840	9	AC093598	C 924	19	1.0	110000	2	AC128128	AC128128	Continuation (2 of
C 852	19	1.0	52000	9	AP002492	C 925	19	1.0	110000	2	AC128128	AC128128	Continuation (2 of
C 853	19	1.0	53025	9	AC118458	C 926	19	1.0	110000	2	AC128128	AC128128	Continuation (2 of
C 854	19	1.0	55589	5	AC087179	C 927	19	1.0	110000	2	AL606505	AL606505	Continuation (2 of
C 855	19	1.0	56086	8	AP004948	C 928	19	1.0	110000	2	AL606505	AL606505	Continuation (2 of
C 856	19	1.0	56891	2	AC101012	C 929	19	1.0	110000	2	BX901936	BX901936	Mus muscu
C 857	19	1.0	57281	2	AC104861	C 930	19	1.0	110000	8	CR380959	CR380959	Continuation (3 of
C 858	19	1.0	57652	2	AC104861	C 931	19	1.0	110000	8	CR382129	CR382129	Continuation (3 of
C 859	19	1.0	59693	9	AC008457	C 932	19	1.0	110000	8	CR382129	CR382129	Continuation (3 of
C 860	19	1.0	60461	2	AC080063	C 933	19	1.0	110000	8	ATAC016829	ATAC016829	Continuation (3 of
C 861	19	1.0	62458	2	AC067878	C 934	19	1.0	111122	8	ATAC016829	ATAC016829	Continuation (3 of
C 862	19	1.0	63123	2	AC137939	C 935	19	1.0	111635	9	AL591027	AL591027	Human DNA
C 863	19	1.0	64198	10	AL611935	C 936	19	1.0	111936	8	AC024260	AC024260	Homo sapi
C 864	19	1.0	64341	10	AL627423	C 937	19	1.0	111936	8	AC024260	AC024260	Homo sapi
C 865	19	1.0	66606	2	AC101404	C 938	19	1.0	112037	10	AL645851	AL645851	Mus muscu
C 866	19	1.0	66425	2	AC110546	C 939	19	1.0	112037	10	AL645851	AL645851	Mus muscu
C 867	19	1.0	68570	2	AC067888	C 940	19	1.0	112885	8	AP005845	AP005845	Homo sapi
C 868	19	1.0	69570	2	AC067888	C 941	19	1.0	112885	8	AP005845	AP005845	Homo sapi
C 869	19	1.0	71151	2	AC128128	C 942	19	1.0	113778	8	BX897674	BX897674	Oryza sat
C 870	19	1.0	71616	8	ATAC022287	C 943	19	1.0	114190	10	AL645842	AL645842	Neurospor
C 871	19	1.0	72172	2	AC010311	C 944	19	1.0	114367	8	ATF10M10	ATF10M10	Arabidops
C 872	19	1.0	72450	2	AC025914	C 945	19	1.0	114817	8	AC149836	AC149836	Zea mays
C 873	19	1.0	74997	10	AL732362	C 946	19	1.0	116803	9	AC131904	AC131904	Homo sapi
C 874	19	1.0	76693	8	AP006368	C 947	19	1.0	117839	8	AC097447	AC097447	Oryza sat
C 875	19	1.0	76808	2	AC014187	C 948	19	1.0	118030	2	AP000667	AP000667	Homo sapi
C 876	19	1.0	78153	3	CEY53C10A	C 949	19	1.0	118472	8	AP003861	AP003861	Oryza sat
C 877	19	1.0	80824	3	AL513480	C 950	19	1.0	118873	9	HS1184F4	HS1184F4	Oryza sat
C 878	19	1.0	82251	9	AC004506	C 951	19	1.0	119037	2	AC040983	AC040983	Mus muscu
C 879	19	1.0	82584	8	NCB13B3	C 952	19	1.0	121524	2	AC144472	AC144472	Felis cat
C 880	19	1.0	84552	9	AC105311	C 953	19	1.0	121684	8	AL354655	AL354655	Homo sapi
C 881	19	1.0	85303	2	AC126918	C 954	19	1.0	121914	8	AC125944	AC125944	Oryza sat
C 882	19	1.0	85567	8	AB016878	C 955	19	1.0	122464	8	AP003858	AP003858	Oryza sat
C 883	19	1.0	86106	8	AB014546	C 956	19	1.0	122571	9	AF064859	AF064859	Homo sapi
C 884	19	1.0	86882	9	AX649553	C 957	19	1.0	122934	9	AC092898	AC092898	Homo sapi
C 885	19	1.0	87379	10	AL845361	C 958	19	1.0	124041	9	CNS01DSD	CNS01DSD	Human chr
C 886	19	1.0	87538	8	AL158200	C 959	19	1.0	125151	9	AC093821	AC093821	Human sapi
C 887	19	1.0	88639	2	AL106831	C 960	19	1.0	125285	9	AC121340	AC121340	Homo sapi
C 888	19	1.0	88872	2	AC004537	C 961	19	1.0	125502	8	AT74420	AT74420	Homo sapi
C 889	19	1.0	89787	2	AC020266	C 962	19	1.0	125637	2	AC141713	AC141713	Arabidops
C 890	19	1.0	92620	8	AB026636	C 963	19	1.0	125787	9	AL645820	AL645820	Human DNA
C 891	19	1.0	93951	8	AC010483	C 964	19	1.0	125787	9	HSJ13817A	HSJ13817A	Human DNA
C 892	19	1.0	95665	8	AF004163	C 965	19	1.0	125862	9	AC026696	AC026696	Homo sapi
C 893	19	1.0	95932	8	AB017060	C 966	19	1.0	126332	8	AC137621	AC137621	Oryza sat
C 894	19	1.0	97410	10	BX465216	C 967	19	1.0	126862	8	AC137507	AC137507	Oryza sat
C 895	19	1.0	97495	9	AC093014	C 968	19	1.0	127286	2	AC025286	AC025286	Homo sapi







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QY 481 AAGAGAAAAGAGAGAGAGAGAGAGATGCTTACTATGTCCTCCGCACTCTCTCT 540
DB 481 AAGAGAAAAGAGAGAGAGAGAGAGAGATGCTTACTATGTCCTCCGCACTCTCTCT 540
QY 541 GGTCCCAAGCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
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QY 901 GCTGTGAGAGAGTTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
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DB 961 GAGATCATGTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
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QY 1081 CATGCGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
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DB 1861 AGCAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1920
QY 1921 GGTATATGAGAGTTCCTCTTTAA 1944
DB 1921 GGTATATGAGAGTTCCTCTTTAA 1944

RESULT 3
AX825705 2189 bp DNA linear PAT 11-DEC-2003
LOCUS AX825705
DEFINITION Sequence 3 from Patent WO03072763.
ACCESSION AX825705
VERSION AX825705.1 GI:39751232
KEYWORDS
SOURCE
ORGANISM
Brassica napus (rape)
Brassica napus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
1 Goring, D., Silva, N. and Hafani, Y.Z.
Increasing plant seed production
Patent: WO 03072763-A 3 04-SEP-2003;
JOURNAL Goring, Daphne (CA) ; Silva, Nancy (CA) ; Hafani, Yosr, Z. (CA)
FEATURES
location/Qualifiers
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1944; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGTCCTGAGGCGCGTCTCGGAGAGTTCGCTTCATCTCAACATCAATCTCACA 60
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QY 61 ACCACCACTCTCTCTCAGAGTTCGCTTCCTCCACACACACCTCTCTCTCGGCG 120
DB 157 ACCACCACTCTCTCTCAGAGTTCGCTTCCTCCACACACACCTCTCTCTCGGCG 216
QY 121 CCATCCATATTCGAGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 180
DB 217 CCATCCATATTCGAGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 276
QY 181 CCATCTCCACCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCA 240
DB 277 CCATCTCCACCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCA 336
QY 241 CCGGCTCAACTAGCGCGGAGATCTTCACCGGACCTGTACTCTCTCTCTCTCTCTCT 300

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Db 337 CCGCTCCAACTACGCGCGGATCTCCACCGGACCTGTATCTCTCTAAGAAACCTT 396  
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 Qy 361 CCATCTTCCCTCCGCGCGCTCTCTTCTTCCAGAGGTTTATCAACAGAGAGTGTGTG 420  
 Db 457 CCATCTTCCCTCCGCGCGCTCTCTTCTTCCAGAGGTTTATCAACAGAGAGTGTGTG 516  
 Qy 421 GGAATGCCATCGAGAGAGT 480  
 Db 517 GGAATGCCATCGAGAGAGT 576  
 Qy 481 AAGAAAGAAAG 540  
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 Db 1357 GCTAAG 1416  
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 Qy 1441 TATGATAG 1500  
 Db 1537 TATGATAG 1596  
 Qy 1501 GGAG 1560  
 Db 1597 GGAG 1656  
 Qy 1561 GCTGCAAG 1620  
 Db 1657 GCTGCAAG 1716  
 Qy 1621 ATGAG 1680  
 Db 1717 ATGAG 1776  
 Qy 1681 ATGAG 1740  
 Db 1777 ATGAG 1836  
 Qy 1741 AGCCAGTCAATGAG 1800  
 Db 1837 AGCCAGTCAATGAG 1896  
 Qy 1801 AACGCCAG 1860  
 Db 1897 AACGCCAG 1956  
 Qy 1861 AGCAG 1920  
 Db 1957 AGCAG 2016  
 Qy 1921 GGTATAG 1944  
 Db 2017 GGTATAG 2040

RESULT 4  
 LOCUS AY028699 2189 bp mRNA linear PIN 26-MAR-2001  
 DEFINITION Brassica napus receptor protein kinase PERK1 mRNA, complete cds.  
 ACCESSION AY028699  
 VERSION AY028699.1 GI:13447448  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Brassica napus (rape)  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.  
 REFERENCE  
 1 (bases 1 to 2189)  
 Silva,N.F. and Goring,D.R.  
 Characterization of a novel Brassica napus receptor protein kinase  
 PERK1  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 2189)  
 AUTHORS Silva,N.F. and Goring,D.R.  
 TITLE Direct Submission  
 JOURNAL Submitted (19-MAR-2001) Biology, York University, 4700 Keele  
 Street, Toronto, Ontario M3J 1P3, Canada  
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Db 1957 AGACGGAGGGCCAAACACACGCGGAATGAGATGGGAGATTAAAGAACCGGTGAG 2016

QY 1921 GGTATAGTGACACTTCTCTTTAA 1944

Db 2017 GGTATAGTGACACTTCTCTTTAA 2040

RESULT 5  
AY536856

LOCUS Arabidopsis thaliana putative protein kinase (At3g24550) mRNA,  
partial cds.

DEFINITION AY536856

ACCESSION AY536856

VERSION AY536856.1 GI:45454229

KEYWORDS

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 668)  
Kurtz, J. and Leister, D.  
Protein kinases in chloroplasts  
Unpublished  
2 (bases 1 to 668)  
Kurtz, J. and Leister, D.  
Direct Submission  
Submitted (22-JAN-2004) Leister Laboratory, Max Planck Institut  
fuern Zuechtungsforchung, Carl-von-Linne Weg 10, Cologne 50829,  
Germany

FEATURES  
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KTGGQ"

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 5e-24;  
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1432 AACATGCTATAGTATGATGACGCTTAGTGACTGGGACGACCATGCTTAACCGAGA 1491

Db 178 AACATGCTATAGTATGATGACGCTTAGTGACTGGGACGACCATGCTTAACCGAGA 237

QY 1492 TCTGAG 1497

Db 238 TCTGAG 243

RESULT 6  
AX825738

LOCUS 1959 bp DNA linear PAT 11-DEC-2003

DEFINITION Sequence 36 from Patent WO03072763.

ACCESSION AX825738

VERSION AX825738.1 GI:39751255

KEYWORDS

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1  
Goring, D., Silva, N. and Haffani, Y. Z.  
Increasing plant seed production  
Patent: WO 03072763-A 36 04-SEP-2003;  
Goring, Daphne (CA); Silva, Nancy (CA); Haffani, Yossr, Z. (CA)

FEATURES  
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 4.7e-24;  
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QY 1492 TCTGAG 1497

Db 1507 TCTGAG 1512

RESULT 7  
BT008400

LOCUS Arabidopsis thaliana At3g24550 gene, complete cds.

DEFINITION BT008400

VERSION BT008400.1 GI:30725473

KEYWORDS

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 1959)  
Cheuk, R., Chen, H., Kim, C.J., Shin, P., Bowser, L., Carninci, P.,  
Dale, J.M., Hayashizaki, Y., Hsuan, Y.W., Ishida, J., Jones, T.,  
Kamuya, A., Karlin-Neumann, G., Kawai, J., Lam, B., Lin, J., Miranda, M.,  
Narusaka, M., Nguyen, M., Onodera, C.S., Palm, C.J., Quach, H.L.,  
Sakurai, T., Satou, M., Seki, M., Southwick, A., Toriumi, M., Wong, C.,  
Wu, H.C., Yamada, K., Yu, G., Yuan, S., Shinozaki, K., Davis, R.W.,  
Thellogis, A. and Ecker, J.R.  
Arabidopsis ORF clones

TITLE

JOURNAL Unpublished

AUTHORS 2 (bases 1 to 1959)  
Cheuk, R., Chen, H., Kim, C.J., Shin, P., Bowser, L., Carninci, P.,  
Dale, J.M., Hayashizaki, Y., Hsuan, Y.W., Ishida, J., Jones, T.,  
Kamuya, A., Karlin-Neumann, G., Kawai, J., Lam, B., Lin, J., Miranda, M.,  
Narusaka, M., Nguyen, M., Onodera, C.S., Palm, C.J., Quach, H.L.,  
Sakurai, T., Satou, M., Seki, M., Southwick, A., Toriumi, M., Wong, C.,  
Wu, H.C., Yamada, K., Yu, G., Yuan, S., Shinozaki, K., Davis, R.W.,  
Thellogis, A. and Ecker, J.R.  
Direct Submission  
Submitted (15-MAY-2003) Salk Institute Genomic Analysis Laboratory  
(SIGAL), Plant Biology Laboratory, The Salk Institute for  
Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,  
USA

COMMENT

The discrepancy does not affect the protein sequence.  
RIKEN Genomic Sciences Center (GSC) members carried out the  
collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN  
Arabidopsis Full-length cDNA'): Seki, M., Narusaka, M., Ishida, J.,  
Satou, M., Kamuya, A., Sakurai, T., Carninci, P., Kawai, J.,  
Hayashizaki, Y. and Shinozaki, K.







## FEATURES

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Location/Qualifiers

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CDS

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3'UTRQuery Match  
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Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1492 TCTGAG 1497

Db 1543 TCTGAG 1548

## ORIGIN

Query Match  
Best Local Similarity 100.0%; Pred. No. 4,7e-24;

Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1432 AACAAATCTATGATGATGACAGCTTAGTACTGCGCAGACCATTCCTTAACCGAGCA 1491

Db 1478 AACAAATCTATGATGATGACAGCTTAGTACTGCGCAGACCATTCCTTAACCGAGCA 1537

QY 1492 TCTGAG 1497

Db 1538 TCTGAG 1543

## REFERENCE

AUTHORS

TITLE  
JOURNAL

COMMENT

USA  
 e-mail for correspondence: arab@sequence.stanford.edu  
 RIKEN Genomic Sciences Center (GSC) members carried out the  
 collection and clustering of RAFL cDNAs (RAFL cDNA: "RIKEN  
 Arabidopsis Full-Length cDNA"): Seki, M., Narusaka, M., Ishida, J.,  
 Satou, M., Kamita, A., Sakurai, T., Carninci, P., Kawai, J.,

Hayashizaki, Y. and Shinozaki, K.

The Sak, Stanford, PGEC (SSP) Consortium members carried out the  
 sequencing and annotation of the RAFL cDNAs: Nguyen, M.,  
 Southwick, A., Karlin-Neumann, G., Lam, B., Miranda, M.,  
 Bowser, L., Jones, T., Bann, J., Chen, H., Cheuk, R., Chung, M. K.,  
 Kim, C., Lin, J., Liu, S. X., Pham, P. K., Sakano, H., Shinn, P.,  
 Yamada, K., Ecker, J., Theologis, A. and Davis, R. W.

Nguyen, M. (SSP/Stanford) and Seki, M. (RIKEN GSC) contributed  
 equally to this work. Shinozaki, K. (RIKEN GSC) and Davis, R. W.  
 (SSP/Stanford) contributed equally to this work as PI.

## FEATURES

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Location/Qualifiers

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CDS

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## RESULT 12

AY093065

LOCUS

Arabidopsis thaliana unknown protein (At3g24550) mRNA, complete

DEFINITION

cde

ACCESSION

AY093065

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

1 (bases 1 to 2190)  
 Southwick, A., Karlin-Neumann, G., Nguyen, M., Lam, B., Miranda, M.,  
 Palm, C. J., Bowser, L., Jones, T., Bann, J., Carninci, P., Chen, H.,  
 Cheuk, R., Chung, M. K., Hayashizaki, Y., Ishida, J., Kamiya, A.,  
 Kawai, J., Kim, C., Lin, J., Liu, S. X., Narusaka, M., Pham, P. K.,



Db 1553 AACATGCTATGATGATACAGCTTAGTGTGACTGGCGACGACCATGCTTACGAGCA 1612  
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 1613 TCTGAG 1618  
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 LOCUS AB020746 79706 bp DNA linear PLN 14-FEB-2004  
 DEFINITION Arabidopsis thaliana genomic DNA, chromosome 3, pl clone: MOB24.  
 ACCESSION AB020746 BA000014  
 VERSION AB020746.1 GI:3985949  
 KEYWORDS  
 SOURCE ORGANISM  
 REFERENCE  
 AUTHORS Kaneo,T., Katoh,T., Sato,S., Nakamura,A., Asamizu,E. and Tabata,S.  
 TITLE Structural analysis of Arabidopsis thaliana chromosome 3. II. Sequence features of the 4,251,695 bp regions covered by 90 Pl, TAC and BAC clones  
 JOURNAL DNA Res. 7 (3), 217-221 (2000)  
 MEDLINE 20363099  
 PUBMED 10907853  
 JOURNAL 2 (bases 1 to 79706)  
 AUTHORS Kaneo,T., Katoh,T., Sato,S., Nakamura,Y., Asamizu,E. and Tabata,S.  
 TITLE Direct Submission  
 JOURNAL Submitted (03-DEC-1998) Yasukazu Nakamura, Kazusa DNA Research Institute, Department of Plant Gene Research, 1512-3, Yana, Kisarazu, Chiba 292-0812, Japan (E-mail: ynakamu@kazusa.or.jp, Tel:81-438-52-3935, Fax:81-438-52-3934)  
 COMMENT  
 Address for correspondence: kaos@kazusa.or.jp  
 For the latest information on annotation of this clone, please see http://www.kazusa.or.jp/kaos/cgi-bin/agd-graph.cgi?c=MOB24  
 Genes with similarity to proteins in the databases are described in 'product' or 'note' qualifiers. Genes that have no significant protein similarity are described as 'unknown protein'.  
 The software programs used to predict genes include: Graal (Informatics Group, Oak Ridge National Laboratory, http://complib.ornl.gov/Graal-1.3/), GENSCAN (Chris Burge, MIT, http://CCR-081.mit.edu/GENSCAN.html), NetGene2 (S.M. Hebsgaard, et al., CBS, Technical University of Denmark, http://www.cbs.dtu.dk/services/NetGene2/) and SplicePredictor (Volker Brendel, Stanford University, http://gremmlin.zool.iastate.edu/cgi-bin/sp.cgi).  
 Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, Washington University School of Medicine, St. Louis, http://genome.wustl.edu/eddy/tRNAscan-SE/).  
 This sequence may not be the entire insert of this clone. It may be shorter because we remove overlaps between neighboring submissions.  
 The 5' clone is MXP5 and the 3' clone is MSD24.  
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Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1579 GCTGGCGCTGTGTGTCGCAATTGAGCTGCGCGAGACCTGCGATGAGCCAG 1629  
Db 54008 GCTGGCGCTGTGTGTCGCAATTGAGCTGCGCGAGACCTGCGATGAGCCAG 54058

RESULT 15  
AY089024  
LOCUS  
DEFINITION  
Arabidopsis thaliana clone 17909 mRNA, complete sequence.  
ACCESSION  
AY089024  
VERSION  
AY089024.1  
KEYWORDS  
FLI CDNA.  
SOURCE  
Arabidopsis thaliana (thale cress)  
ORGANISM  
Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
1 (bases 1 to 2324)  
Haas, B.J., Volfovsky, N., Town, C.D., Troukhan, M., Alexandrov, N.,  
Feldmann, K.A., Flavell, R.B., White, O., and Salzberg, S.L.  
Full-length messenger RNA sequences greatly improve genome  
annotation  
Genome Biol. 3 (6), RESEARCH0029 (2002)  
22088475  
MEDLINE  
PUBMED  
12093376  
2 (bases 1 to 2324)  
Broyer, V., Troukhan, M., Alexandrov, N., Lu, Y.-P., Flavell, R. and  
Feldmann, K.  
Full-length cDNA from Arabidopsis thaliana  
Unpublished  
3 (bases 1 to 2324)  
Broyer, V., Troukhan, M., Alexandrov, N., Lu, Y.-P., Flavell, R. and  
Feldmann, K.  
Direct Submision  
Submitted (11-MAR-2002) Ceres, Inc, 3007 Malibu Canyon Road,  
Malibu, CA 90265, USA  
This clone sequence is one of 5,000 Ceres full-length cDNAs made  
available to TIGR and Genbank. The following quality assessment of  
this set was done by comparison with known proteins: two percent of  
the clones are estimated to be 5'-truncated; less than one percent  
are 3'-truncated; approximately two percent represent alternative  
splice variants, including unspliced introns and spliced exons; one  
percent may contain premature stop codons; five percent may have  
frame shifts in a coding region. A sequence is considered to be  
5'-truncated if it lacks the translation initiation start (ATG). A  
sequence is considered to be 3'-truncated if it lacks the  
C-terminal end of the encoded protein. Please note that these cDNA  
sequences are derived from the Ws or later ecotypes and therefore  
may contain polymorphisms when compared to sequences from Col-0.  
Genet carried out the library production and sequencing of the  
full-length clones. Ceres, Inc. carried out the clustering of the  
5' sequences, selection of clones, and sequence assembly.  
Location/Qualifiers  
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ORIGIN

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Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1585 GCTTGTGTCGCAATTGAGCTGCGCGAGACCTGCGATGAGCCAGAT 1631  
Db 1700 GCTTGTGTCGCAATTGAGCTGCGCGAGACCTGCGATGAGCCAGAT 1746

Search completed: November 13, 2004, 14:21:32  
Job time : 5615 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 13, 2004, 10:56:30 ; Search time 651 Seconds

(without alignment)  
15675.690 Million cell updates/sec

Title: US-10-069-304-1

Perfect score: 1944

Sequence: 1 atgctctcggcgccgctctcc.....atagtggaacctctcttaaa 1944

Scoring table:

OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 4134866 seqs, 2624710521 residues

Word size : 0

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database :

N\_Geneseq\_23Sep04:\*  
1: geneseqn1980s:\*  
2: geneseqn1990s:\*  
3: geneseqn2000s:\*  
4: geneseqn2001as:\*  
5: geneseqn2001bs:\*  
6: geneseqn2002as:\*  
7: geneseqn2002bs:\*  
8: geneseqn2003as:\*  
9: geneseqn2003bs:\*  
10: geneseqn2003cs:\*  
11: geneseqn2003ds:\*  
12: geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	1944	100.0	1944	10	ACF36548
3	1944	100.0	2189	10	ACF36549
4	66	3.4	1959	10	ACF36557
5	47	2.4	2324	3	AAc36968
6	27	1.4	685	10	ADK53814
7	26	1.3	1515	9	ACF36555
8	26	1.3	110000	3	AAf22305_06
9	26	1.3	110000	3	AAf22305_07
10	24	1.2	1389	8	ADf70853
11	24	1.2	1515	9	ADf70853
12	24	1.2	1515	9	ADf70853
13	24	1.2	1515	9	ADf70853
14	24	1.2	1515	9	ADf70853
15	24	1.2	1515	9	ADf70853
16	23	1.2	579	12	ACH93299
17	23	1.2	897	10	ACH93299
18	23	1.2	897	10	ACH93299
19	23	1.2	897	10	ACH93299
20	23	1.2	1005	10	ACH93299
21	23	1.2	1281	10	ACH93299

22	1.2	1572	5	AAf77094	Brassica
23	1.2	3252	10	ACF36548	B. napus
24	1.2	4173	10	ACF36549	B. napus
25	1.2	4517	6	ACF36557	B. napus
26	1.2	4586	8	AAc36968	Arabidopsis
27	1.2	4586	12	ADK53814	Plant DNA
28	1.2	4620	10	ACF36555	Z. mays
29	1.2	4620	10	AAf22305_06	Continuation (7 of
30	1.2	4620	10	AAf22305_07	Continuation (8 of
31	1.2	4620	12	ACH93299	Human gene
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C 96	20	1.0	5769	4	ABA06468	Abao6468 Human cdn	C 169	19	1.0	2421	3	AAD00747	Aad00747 Mouse Act
C 97	20	1.0	5769	6	ABV83805	Abv83805 Human pol	C 170	19	1.0	2430	4	AAH27430	Aah27430 Human UDP
C 98	20	1.0	5868	3	AAA28019	Aaa28019 Quelling	C 171	19	1.0	2487	3	AAD00748	Aad00748 Mouse Act
C 99	20	1.0	6916	3	AAA28019	Aaa28019 Quelling	C 172	19	1.0	2487	3	AAD00748	Aad00748 Mouse Act
C 100	20	1.0	7142	6	ABSS8372	Abss8372 Protein m	C 173	19	1.0	2746	4	AAH18149	Aah18149 Human cdn
C 101	20	1.0	8029	3	AAI62036	Aai62036 Human cel	C 174	19	1.0	2820	4	AAH18149	Aah18149 Human cdn
C 102	20	1.0	41100	4	AAI10873	Aai10873 Human gen	C 175	19	1.0	2820	4	AAH18149	Aah18149 Human cdn
C 103	20	1.0	97700	10	ADLI3678	Adli3678 Streptococ	C 176	19	1.0	3517	10	ADB61948	Adb61948 Human cdn
C 104	20	1.0	305107	4	AAH62689	Aah62689 Strimp wh	C 177	19	1.0	3517	10	ADB61948	Adb61948 Human cdn
C 105	19	1.0	105	12	ACH81173	Ach81173 Human gen	C 178	19	1.0	3600	10	AAD62490	Aad62490 N-acetylgl
C 106	19	1.0	141	12	ACH82031	Ach82031 Human gen	C 179	19	1.0	3600	10	AAD62490	Aad62490 N-acetylgl
C 107	19	1.0	189	8	ACC84440	Acc84440 Clone T11	C 180	19	1.0	3621	4	ACC81011	Acc81011 Human Glc
C 108	19	1.0	189	9	ACC47443	Acc47443 Nucleotid	C 181	19	1.0	3621	4	ACC81011	Acc81011 Human Glc
C 109	19	1.0	268	12	ADP95597	Adp95597 Cotion ex	C 182	19	1.0	3783	6	ABR84074	AbR84074 Human Glc
C 110	19	1.0	268	6	ABL76899	AbL76899 L. paracas	C 183	19	1.0	3831	4	ABL04737	AbL04737 Drosophi
C 111	19	1.0	323	2	AAK88282	Aak88282 Human dig	C 184	19	1.0	3831	4	ABL04737	AbL04737 Drosophi
C 112	19	1.0	323	5	AAAS39429	Aas39429 cDNA enco	C 185	19	1.0	3879	4	ABL28657	AbL28657 Drosophi
C 113	19	1.0	333	9	ADB32155	AdB32155 Human nov	C 186	19	1.0	4080	8	ABL28136	AbL28136 Drosophi
C 114	19	1.0	333	2	AAT11309	Aat11309 Allergen	C 187	19	1.0	4174	4	ABL28076	AbL28076 Drosophi
C 115	19	1.0	358	2	AAK83357	Aak83357 Breast ca	C 188	19	1.0	4176	6	ABO61063	AbO61063 Drosophi
C 116	19	1.0	358	2	AAV68897	Aav68897 DNA molec	C 189	19	1.0	4277	6	ADA41203	Ada41203 Human nuc
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C 120	19	1.0	358	8	ADA11247	Ada11247 Human bre	C 193	19	1.0	4624	4	ABL03466	AbL03466 Drosophi
C 121	19	1.0	358	10	ADCI5220	Adci5220 Human bre	C 194	19	1.0	4977	8	ABZ78161	AbZ78161 Human can
C 122	19	1.0	423	8	ABX42341	Abx42341 Bovine ES	C 195	19	1.0	5042	6	ABN56966	AbN56966 Novel hum
C 123	19	1.0	437	3	AAC02784	Aac02784 Human sec	C 196	19	1.0	5053	4	AAF60732	Aaf60732 Rat UG9T
C 124	19	1.0	463	4	AAI15613	Aai15613 Probe #55	C 197	19	1.0	5225	8	ABZ78162	AbZ78162 Human can
C 125	19	1.0	463	4	AAI15610	Aai15610 Human foe	C 198	19	1.0	5225	8	ABZ78162	AbZ78162 Human can
C 126	19	1.0	463	4	AAI37172	Aai37172 Probe #58	C 199	19	1.0	5252	12	ADQ21455	AdQ21455 Human sol
C 127	19	1.0	463	4	ABA27043	AbA27043 Probe #55	C 200	19	1.0	5285	12	ADQ25300	AdQ25300 Human sol
C 128	19	1.0	463	4	AAK31273	Aak31273 Human bon	C 201	19	1.0	5362	10	ADBO6975	AdBo6975 Novel cod
C 129	19	1.0	463	4	AAK05663	Aak05663 Human bra	C 202	19	1.0	5597	4	ACC81001	Acc81001 Human Glc
C 130	19	1.0	463	4	ABSS0953	Abss0953 Human liv	C 203	19	1.0	5597	10	ADD27811	Add27811 Human Glc
C 131	19	1.0	463	6	ABSO6025	Abso6025 Human gen	C 204	19	1.0	5597	10	ADD27811	Add27811 Human Glc
C 132	19	1.0	465	9	ACH38230	Ach38230 Human end	C 205	19	1.0	6616	6	ABL32475	AbL32475 Human jmm
C 133	19	1.0	485	5	AAAS84001	Aas84001 DNA enco	C 206	19	1.0	6625	4	ABL19750	AbL19750 Drosophi
C 134	19	1.0	494	9	ACH35924	Ach35924 Human end	C 207	19	1.0	6754	6	ABL19750	AbL19750 Drosophi
C 135	19	1.0	498	8	ACC5440	Acc5440 Rice endo	C 208	19	1.0	6754	6	ABL19750	AbL19750 Drosophi
C 136	19	1.0	531	4	AAI24837	Aai24837 Probe #14	C 209	19	1.0	7182	9	ACH04002	Ach04002 Human gen
C 137	19	1.0	531	4	ABA70232	AbA70232 Human foe	C 210	19	1.0	8810	10	ADG39793	AdG39793 Human can
C 138	19	1.0	531	4	AAI50362	Aai50362 Probe #15	C 211	19	1.0	8810	10	ADG39793	AdG39793 Human can
C 139	19	1.0	531	4	AAA36361	Aaa36361 Probe #15	C 212	19	1.0	9567	6	ABSS6501	Abss6501 Invertebr
C 140	19	1.0	531	4	AAK18458	Aak18458 Human bra	C 213	19	1.0	9567	6	ABSS6501	Abss6501 Invertebr
C 141	19	1.0	531	4	ABSA4020	AbSA4020 Human liv	C 214	19	1.0	9574	6	AAD39238	Aad39238 Fruit fly
C 142	19	1.0	531	6	ABSI8599	AbSI8599 Human gen	C 215	19	1.0	9574	6	AAD39238	Aad39238 Fruit fly
C 143	19	1.0	533	12	ACH79758	Ach79758 Human gen	C 216	19	1.0	12839	4	ABL10164	AbL10164 Drosophi
C 144	19	1.0	533	12	ACH68330	Ach68330 Human gen	C 217	19	1.0	13514	4	ABL04736	AbL04736 Drosophi
C 145	19	1.0	533	12	ACH67469	Ach67469 Human gen	C 218	19	1.0	16579	10	ADB54118	AdB54118 Human can
C 146	19	1.0	594	12	AAAC1544	AaA1544 Rice gene	C 219	19	1.0	16579	10	ADB53965	AdB53965 Human TPE
C 147	19	1.0	615	8	ADA70472	Ada70472 Rice gene	C 220	19	1.0	16579	10	ADB53965	AdB53965 Human TPE
C 148	19	1.0	629	4	AAK90133	Aak90133 Human dig	C 221	19	1.0	16579	10	ADB53965	AdB53965 Human TPE
C 149	19	1.0	629	5	AAAS39780	Aas39780 Genomic s	C 222	19	1.0	16579	10	ADB53965	AdB53965 Human TPE
C 150	19	1.0	629	5	AAAS39780	Aas39780 Genomic s	C 223	19	1.0	16579	10	ADB53965	AdB53965 Human TPE
C 151	19	1.0	629	5	ADH32740	Adh32740 Human nov	C 224	19	1.0	16579	10	ADB53965	AdB53965 Human TPE
C 152	19	1.0	635	12	ADJ40578	Adj40578 Plant CDN	C 225	19	1.0	110000	8	ABX16390_5	AbX16390_5 of
C 153	19	1.0	636	3	AAAC36993	AaA36993 Arabidops	C 226	19	1.0	110000	8	ABX16390_5	AbX16390_5 of
C 154	19	1.0	650	6	AAQ65553	AaQ65553 Arabidops	C 227	19	1.0	110000	8	ABX16390_5	AbX16390_5 of
C 155	19	1.0	826	5	AAQ65553	AaQ65553 Arabidops	C 228	19	1.0	110000	8	ABX16390_5	AbX16390_5 of
C 156	19	1.0	833	4	AAI96515	Aai96515 Human neu	C 229	19	1.0	147	9	ADA48473	Ada48473 Rice gene
C 157	19	1.0	833	4	AAI96515	Aai96515 Human neu	C 230	19	1.0	147	9	ADA48473	Ada48473 Rice gene
C 158	19	1.0	899	8	AAAC51829	AaA51829 Arabidops	C 231	19	1.0	195	6	ABL85971	AbL85971 Human ova
C 159	19	1.0	909	8	ABX92196	Abx92196 Human ova	C 232	19	1.0	201	6	ABL85975	AbL85975 Human ova
C 160	19	1.0	985	4	AAH01965	Aah01965 Candida z	C 233	19	1.0	201	6	ABL85975	AbL85975 Human ova
C 161	19	1.0	1025	12	AD062054	Ad062054 Transcript	C 234	19	1.0	203	4	ABD23500	AbD23500 Human lun
C 162	19	1.0	1046	3	AAAC35608	AaA35608 Arabidops	C 235	19	1.0	203	4	ABD23500	AbD23500 Human lun
C 163	19	1.0	1306	3	AAAC32002	AaA32002 Arabidops	C 236	19	1.0	203	4	ABD23500	AbD23500 Human lun
C 164	19	1.0	1704	8	ADA69514	Ada69514 Rice gene	C 237	19	1.0	203	4	ABD23500	AbD23500 Human lun
C 165	19	1.0	1947	10	ADP09611	AdP09611 Human pap	C 238	19	1.0	209	6	ABL85687	AbL85687 Human ova
C 166	19	1.0	2009	8	ADA72436	Ada72436 Rice gene	C 239	19	1.0	216	4	AAI22855	Aai22855 Probe #12
C 167	19	1.0	2238	5	AAH90033	Aah90033 Human Don	C 240	19	1.0	216	4	AAI22855	Aai22855 Probe #12
C 167	19	1.0	2238	5	AAH90033	Aah90033 Human Don	C 240	19	1.0	216	4	AAI22855	Aai22855 Probe #12
C 167	19	1.0	2238	5	AAH90033	Aah90033 Human Don	C 240	19	1.0	216	4	AAI22855	Aai22855 Probe #12

C 241	18	0.9	216	4	AAI48155	AAI48155	Probe #16	C 314	18	0.9	375	4	ABS38806	ABS38806	Human liv
C 242	18	0.9	216	4	ABA50021	ABA50021	Human bre	C 315	18	0.9	375	5	AAI05738	AAI05738	Probe #57
C 243	18	0.9	216	4	ABA49899	ABA49899	Probe #13	C 316	18	0.9	375	5	ABS13305	ABS13305	Human gen
C 244	18	0.9	216	4	AAK42089	AAK42089	Human bon	C 317	18	0.9	378	12	ADP92453	ADP92453	Cotton ex
C 245	18	0.9	216	4	AAK16339	AAK16339	Human bra	C 318	18	0.9	382	4	AAK36951	AAK36951	Novel hum
C 246	18	0.9	216	4	ABS41695	ABS41695	Human liv	C 319	18	0.9	386	12	ADP94904	ADP94904	Cotton ex
C 247	18	0.9	216	5	AAI08524	AAI08524	Probe #65	C 320	18	0.9	393	5	AAK30684	AAK30684	DNA encod
C 248	18	0.9	216	6	ABS16131	ABS16131	Human gen	C 321	18	0.9	439	6	ABR07111	ABR07111	Human ova
C 249	18	0.9	227	4	AAI22239	AAI22239	Probe #12	C 322	18	0.9	439	8	ABK72989	ABK72989	Human ova
C 250	18	0.9	227	4	ABA67317	ABA67317	Human foe	C 323	18	0.9	447	5	AAK3684	AAK3684	Human ova
C 251	18	0.9	227	4	AAI47532	AAI47532	Probe #16	C 324	18	0.9	447	5	AAK3684	AAK3684	Human ova
C 252	18	0.9	227	4	ABA49406	ABA49406	Human bre	C 325	18	0.9	447	12	ADL30111	ADL30111	DNA encod
C 253	18	0.9	227	4	ABA34408	ABA34408	Probe #12	C 326	18	0.9	450	4	ABA59302	ABA59302	Human foe
C 254	18	0.9	227	4	AAK41491	AAK41491	Human bon	C 327	18	0.9	450	4	AAK39102	AAK39102	Probe #77
C 255	18	0.9	227	4	AAK15752	AAK15752	Human bra	C 328	18	0.9	450	4	AAK3313	AAK3313	Human bon
C 256	18	0.9	227	4	ABS41080	ABS41080	Human liv	C 329	18	0.9	450	4	AAK07521	AAK07521	Human bra
C 257	18	0.9	227	5	AAI07937	AAI07937	Probe #79	C 330	18	0.9	450	4	ABS33066	ABS33066	Human liv
C 258	18	0.9	227	5	ABS15496	ABS15496	Human gen	C 331	18	0.9	450	4	ABS08148	ABS08148	Human gen
C 259	18	0.9	259	2	AAV90205	AAV90205	EST clone	C 332	18	0.9	453	6	ABR22857	ABR22857	Drosophila
C 260	18	0.9	262	6	ABR85880	ABR85880	Human ova	C 333	18	0.9	459	9	ABR44328	ABR44328	DNA clone
C 261	18	0.9	265	5	ABV58299	ABV58299	Human pro	C 334	18	0.9	464	5	ABR44328	ABR44328	DNA clone
C 262	18	0.9	265	5	ABV58274	ABV58274	Human pro	C 335	18	0.9	464	5	ABR44328	ABR44328	DNA clone
C 263	18	0.9	270	6	ABR85716	ABR85716	Human ova	C 336	18	0.9	464	5	ABR44328	ABR44328	DNA clone
C 264	18	0.9	272	12	ADJ67287	ADJ67287	Human ova	C 337	18	0.9	464	5	ABR44328	ABR44328	DNA clone
C 265	18	0.9	272	10	ABX83800	ABX83800	Human ova	C 338	18	0.9	464	10	ADK57394	ADK57394	Plant DNA
C 266	18	0.9	278	6	ABK79189	ABK79189	Bacillus	C 339	18	0.9	465	4	AAI25521	AAI25521	Probe #15
C 267	18	0.9	284	6	ABR172234	ABR172234	Corn tass	C 340	18	0.9	465	4	ABR171691	ABR171691	Human foe
C 268	18	0.9	284	3	AAK43447	AAK43447	Mouse sec	C 341	18	0.9	465	4	AAI51993	AAI51993	Probe #20
C 269	18	0.9	288	12	ADJ67288	ADJ67288	Human ova	C 342	18	0.9	465	4	AAK37800	AAK37800	Probe #16
C 270	18	0.9	293	6	ABX87930	ABX87930	Corn ear-	C 343	18	0.9	465	4	AAK46085	AAK46085	Human bon
C 271	18	0.9	297	10	ABR174547	ABR174547	Corn tass	C 344	18	0.9	465	4	AAK20041	AAK20041	Human bra
C 272	18	0.9	300	6	ABR172346	ABR172346	Corn tass	C 345	18	0.9	465	6	ABS20382	ABS20382	Human liv
C 273	18	0.9	300	10	ABX86248	ABX86248	Corn ear-	C 346	18	0.9	470	4	AAI12522	AAI12522	Human gen
C 274	18	0.9	303	5	AAI19497	AAI19497	Corn ear-	C 347	18	0.9	470	4	ABR54429	ABR54429	Probe #24
C 275	18	0.9	306	5	AAI19497	AAI19497	Corn ear-	C 348	18	0.9	470	4	AAI13875	AAI13875	Human foe
C 276	18	0.9	306	10	ABX85619	ABX85619	Zea mays	C 349	18	0.9	470	4	ABR433770	ABR433770	Probe #25
C 277	18	0.9	308	10	ABX86540	ABX86540	Corn ear-	C 350	18	0.9	470	4	ABR433770	ABR433770	Probe #25
C 278	18	0.9	313	5	ABV14434	ABV14434	Corn ear-	C 351	18	0.9	470	4	AAK27943	AAK27943	Probe #24
C 279	18	0.9	321	3	ADP57032	ADP57032	Human pro	C 352	18	0.9	470	4	AAK27943	AAK27943	Probe #24
C 280	18	0.9	331	5	ABV23323	ABV23323	Human pro	C 353	18	0.9	470	4	ABS27525	ABS27525	Human bon
C 281	18	0.9	331	5	ABV229173	ABV229173	Human pro	C 354	18	0.9	470	5	AAI02430	AAI02430	Human bra
C 282	18	0.9	340	6	AAV29348	AAV29348	Human pro	C 355	18	0.9	470	6	ABS02404	ABS02404	Human gen
C 283	18	0.9	340	6	ABR84214	ABR84214	Calcium i	C 356	18	0.9	474	4	AAI11715	AAI11715	Probe #36
C 284	18	0.9	347	3	AAH30839	AAH30839	Human ova	C 357	18	0.9	474	4	AAI11715	AAI11715	Probe #36
C 285	18	0.9	350	3	AAH30940	AAH30940	Human col	C 358	18	0.9	474	4	AAI11715	AAI11715	Probe #36
C 286	18	0.9	355	3	ABV05265	ABV05265	Human pro	C 359	18	0.9	474	4	ABR55425	ABR55425	Human foe
C 287	18	0.9	357	6	ABN78952	ABN78952	Human ORF	C 360	18	0.9	474	4	AAI35071	AAI35071	Probe #17
C 288	18	0.9	360	4	ABA69977	ABA69977	Human foe	C 361	18	0.9	474	4	AAI35071	AAI35071	Probe #17
C 289	18	0.9	360	4	ABA71815	ABA71815	Human foe	C 362	18	0.9	474	4	ABA43033	ABA43033	Human bre
C 290	18	0.9	360	4	AAI50089	AAI50089	Human foe	C 363	18	0.9	474	4	ABA44949	ABA44949	Human bre
C 291	18	0.9	360	4	AAI52158	AAI52158	Probe #18	C 364	18	0.9	474	4	ABA44949	ABA44949	Human bre
C 292	18	0.9	360	4	AAK46257	AAK46257	Human bon	C 365	18	0.9	474	4	ABA23129	ABA23129	Probe #16
C 293	18	0.9	360	4	AAK44079	AAK44079	Human bon	C 366	18	0.9	474	4	ABA23129	ABA23129	Probe #16
C 294	18	0.9	360	4	AAK18186	AAK18186	Human bon	C 367	18	0.9	474	4	AAK27169	AAK27169	Probe #36
C 295	18	0.9	360	4	ABS45979	ABS45979	Human bra	C 368	18	0.9	474	4	AAK29124	AAK29124	Human bon
C 296	18	0.9	360	4	ABS45979	ABS45979	Human bra	C 369	18	0.9	474	4	AAK01717	AAK01717	Human bon
C 297	18	0.9	360	6	ABS20571	ABS20571	Human gen	C 370	18	0.9	474	4	ABS28745	ABS28745	Human bra
C 298	18	0.9	360	6	ABS18313	ABS18313	Human gen	C 371	18	0.9	474	4	ABS28745	ABS28745	Human bra
C 299	18	0.9	360	6	ABS20571	ABS20571	Human gen	C 372	18	0.9	474	5	AAI01684	AAI01684	Human liv
C 300	18	0.9	361	4	AAK35824	AAK35824	Human gen	C 373	18	0.9	474	5	AAI03592	AAI03592	Probe #35
C 301	18	0.9	361	4	AAK35826	AAK35826	Human car	C 374	18	0.9	474	6	ABS01720	ABS01720	Human gen
C 302	18	0.9	361	10	ADRA6518	ADRA6518	Human car	C 375	18	0.9	474	6	ABS01720	ABS01720	Human gen
C 303	18	0.9	361	10	ADRA6520	ADRA6520	Human car	C 376	18	0.9	477	4	AAI10789	AAI10789	Human gen
C 304	18	0.9	362	4	AAK35825	AAK35825	Human car	C 377	18	0.9	477	4	AAI10789	AAI10789	Human gen
C 305	18	0.9	362	10	ADRA6519	ADRA6519	Human car	C 378	18	0.9	477	4	ABR54336	ABR54336	Human gen
C 306	18	0.9	362	12	ADP92107	ADP92107	Cotton ex	C 379	18	0.9	477	4	ABR58376	ABR58376	Human gen
C 307	18	0.9	375	4	AAI20031	AAI20031	Probe #99	C 380	18	0.9	477	4	AAI138009	AAI138009	Human foe
C 308	18	0.9	375	4	ABR45059	ABR45059	Human foe	C 381	18	0.9	477	4	AAI132047	AAI132047	Probe #66
C 309	18	0.9	375	4	AAI45229	AAI45229	Probe #13	C 382	18	0.9	477	4	ABR42018	ABR42018	Human bra
C 310	18	0.9	375	4	ABR47175	ABR47175	Human bre	C 383	18	0.9	477	4	ABR422382	ABR422382	Human bra
C 311	18	0.9	375	4	AAK32165	AAK32165	Probe #10	C 384	18	0.9	477	4	ABR427488	ABR427488	Probe #59
C 312	18	0.9	375	4	AAK39221	AAK39221	Human bon	C 385	18	0.9	477	4	AAK26159	AAK26159	Human bon
C 313	18	0.9	375	4	AAK13482	AAK13482	Human bra	C 386	18	0.9	477	4	AAK32160	AAK32160	Human bra
													AAK06479	AAK06479	Human bra

C 387	18	0.9	477	4	AAK00707	AAK00707 Human bra	C 460	18	0.9	541	3	AAc69779	AAc69779 Human bra
C 388	18	0.9	477	4	ABs31856	ABs31856 Human l1v	C 461	18	0.9	542	6	ABO45536	ABq45536 Oligonuc1
C 389	18	0.9	477	4	ABs25748	ABs25748 Human l1v	C 462	18	0.9	542	6	ABO45537	ABq45537 Oligonuc1
C 390	18	0.9	477	5	AAI00714	AAI00714 Probe #70	C 463	18	0.9	550	6	AB199315	AB199315 Mouse isc
C 391	18	0.9	477	6	ABs00744	ABs00744 Human gen	C 464	18	0.9	564	12	ACH73400	AB121817 Drosoph1l
C 392	18	0.9	477	6	ABs06927	ABs06927 Human gen	C 465	18	0.9	569	4	AAK92276	ACH73400 Human gen
C 393	18	0.9	479	4	AAI13632	AAI13632 Probe #35	C 466	18	0.9	569	4	AAK93997	AAK93997 Human cdn
C 394	18	0.9	479	4	ABs55343	ABs55343 Human foe	C 467	18	0.9	569	4	AAK93997	AAK93997 Human cdn
C 395	18	0.9	479	4	AAI14992	AAI14992 Probe #36	C 468	18	0.9	569	12	ADL28703	ADL28703 5' end of
C 396	18	0.9	479	4	ABs44880	ABs44880 Human bra	C 469	18	0.9	569	12	ADL28703	ADL28703 5' end of
C 397	18	0.9	479	4	ABs44880	ABs44880 Probe #35	C 470	18	0.9	574	9	ACLI6733	ACLI6733 DNA clone
C 398	18	0.9	479	4	AAK29044	AAK29044 Human bon	C 471	18	0.9	574	9	ACLI6733	ACLI6733 DNA clone
C 399	18	0.9	479	4	AAK29044	AAK29044 Human bra	C 472	18	0.9	578	4	AAI12190	AAI12190 Human bra
C 400	18	0.9	479	4	ABs28659	ABs28659 Human l1v	C 473	18	0.9	579	3	AAc77332	AAc77332 Human ORF
C 401	18	0.9	479	5	AAI03516	AAI03516 Probe #35	C 474	18	0.9	584	3	ACLI6732	ACLI6732 DNA clone
C 402	18	0.9	479	6	ABs03589	ABs03589 Human gen	C 475	18	0.9	586	12	ACH67835	ACH67835 Human gen
C 403	18	0.9	482	9	ACLI6725	ACLI6725 DNA clone	C 476	18	0.9	587	9	ACLI6732	ACLI6732 DNA clone
C 404	18	0.9	482	9	AAI16341	AAI16341 Probe #62	C 477	18	0.9	598	12	ACH70271	ACH70271 Human gen
C 405	18	0.9	486	4	ABs59169	ABs59169 Human foe	C 478	18	0.9	623	9	ACLI6733	ACLI6733 DNA clone
C 406	18	0.9	486	4	AAI18923	AAI18923 Probe #64	C 479	18	0.9	631	9	ACLI6733	ACLI6733 DNA clone
C 407	18	0.9	486	4	ABs27939	ABs27939 Probe #64	C 480	18	0.9	633	9	ACLI6729	ACLI6729 DNA clone
C 408	18	0.9	486	4	AAK33127	AAK33127 Human bon	C 481	18	0.9	633	9	ACLI6729	ACLI6729 DNA clone
C 409	18	0.9	486	4	AAK07360	AAK07360 Human bra	C 482	18	0.9	639	9	ACLI6735	ACLI6735 DNA clone
C 410	18	0.9	486	4	ABs32865	ABs32865 Human l1v	C 483	18	0.9	643	3	AAc33333	AAc33333 Arabidops
C 411	18	0.9	486	6	ABs07945	ABs07945 Human gen	C 484	18	0.9	647	9	ACLI6731	ACLI6731 DNA clone
C 412	18	0.9	486	10	ADL16727	ADL16727 DNA (Seq1	C 485	18	0.9	649	9	ACLI6732	ACLI6732 DNA clone
C 413	18	0.9	486	10	ADK58883	ADK58883 Plant DNA	C 486	18	0.9	652	12	ADL12937	ADL12937 Human ste
C 414	18	0.9	489	2	AAQ34771	AAQ34771 PCENP-B-1	C 487	18	0.9	674	3	AAI14190	AAI14190 Aspergill
C 415	18	0.9	494	4	AAI13001	AAI13001 Probe #29	C 488	18	0.9	674	12	ADs77096	ADs77096 Human cdn
C 416	18	0.9	494	4	ABs45701	ABs45701 Human foe	C 489	18	0.9	682	9	ACLI6716	ACLI6716 DNA clone
C 417	18	0.9	494	4	AAI34356	AAI34356 Probe #30	C 490	18	0.9	684	2	ADRL01980	ADRL01980 A. gossyp
C 418	18	0.9	494	4	ABs44252	ABs44252 Human bra	C 491	18	0.9	697	9	ACLI6717	ACLI6717 DNA clone
C 419	18	0.9	494	4	ABs24481	ABs24481 Probe #29	C 492	18	0.9	700	9	ACLI6721	ACLI6721 DNA clone
C 420	18	0.9	494	4	AAK28433	AAK28433 Human bon	C 493	18	0.9	702	9	ACLI6736	ACLI6736 DNA clone
C 421	18	0.9	494	4	AAK02986	AAK02986 Human bra	C 494	18	0.9	718	6	ABs77252	ABs77252 Pirog embr
C 422	18	0.9	494	4	ABs28028	ABs28028 Human l1v	C 495	18	0.9	746	6	ABs77252	ABs77252 Pirog embr
C 423	18	0.9	494	5	AAI02918	AAI02918 Probe #29	C 496	18	0.9	758	11	ADL11793	ADL11793 Rice CDNA
C 424	18	0.9	494	5	ABs02941	ABs02941 Human gen	C 497	18	0.9	801	11	ADL11439	ADL11439 Rice DNA
C 425	18	0.9	496	4	ABs57350	ABs57350 Human foe	C 498	18	0.9	819	5	AAK68928	AAK68928 DNA encod
C 426	18	0.9	496	4	AAI36894	AAI36894 Probe #55	C 499	18	0.9	823	4	AAH03659	AAH03659 Human cdn
C 427	18	0.9	496	4	AAK03982	AAK03982 Human bon	C 500	18	0.9	835	4	AAI21073	AAI21073 Human bra
C 428	18	0.9	496	4	AAK05386	AAK05386 Human bra	C 501	18	0.9	839	6	ABK79237	ABK79237 Bacillus
C 429	18	0.9	496	4	ABs30660	ABs30660 Human l1v	C 502	18	0.9	847	5	AAK59091	AAK59091 DNA encod
C 430	18	0.9	496	6	ABs05731	ABs05731 Human gen	C 503	18	0.9	847	5	AAK59091	AAK59091 DNA encod
C 431	18	0.9	498	10	ADs76237	ADs76237 Human BSK	C 504	18	0.9	853	3	AAK48249	AAK48249 Arabidops
C 432	18	0.9	508	9	ACLI6737	ACLI6737 DNA clone	C 505	18	0.9	854	6	ABZ14401	ABZ14401 Arabidops
C 433	18	0.9	511	4	AAI20967	AAI20967 Probe #10	C 506	18	0.9	861	4	AAI67448	AAI67448 Nucleotid
C 434	18	0.9	511	4	AAI22936	AAI22936 Probe #12	C 507	18	0.9	890	12	ACH87267	ACH87267 Human gen
C 435	18	0.9	511	4	ABs68026	ABs68026 Human foe	C 508	18	0.9	903	3	AAK52125	AAK52125 Arabidops
C 436	18	0.9	511	4	ABs66036	ABs66036 Human foe	C 509	18	0.9	977	3	AAK52125	AAK52125 Arabidops
C 437	18	0.9	511	4	AAI48232	AAI48232 Probe #16	C 510	18	0.9	1002	5	AAK52125	AAK52125 Arabidops
C 438	18	0.9	511	4	AAI46214	AAI46214 Probe #14	C 511	18	0.9	1008	6	AAK52125	AAK52125 Arabidops
C 439	18	0.9	511	4	ABs48160	ABs48160 Human bra	C 512	18	0.9	1014	10	ADA56193	ADA56193 Human cdn
C 440	18	0.9	511	4	ABs50088	ABs50088 Human bra	C 513	18	0.9	1014	10	ADA56193	ADA56193 Human cdn
C 441	18	0.9	511	4	ABs33121	ABs33121 Probe #11	C 514	18	0.9	1014	10	ADA56193	ADA56193 Human cdn
C 442	18	0.9	511	4	ABs35064	ABs35064 Probe #13	C 515	18	0.9	1014	10	ADA56193	ADA56193 Human cdn
C 443	18	0.9	511	4	AAK40199	AAK40199 Human bon	C 516	18	0.9	1014	10	ADA56193	ADA56193 Human cdn
C 444	18	0.9	511	4	AAK142167	AAK142167 Human bra	C 517	18	0.9	1014	10	ADA56193	ADA56193 Human cdn
C 445	18	0.9	511	4	AAK14460	AAK14460 Human bra	C 518	18	0.9	1014	10	ADA56193	ADA56193 Human cdn
C 446	18	0.9	511	4	AAK16420	AAK16420 Human l1v	C 519	18	0.9	1014	10	ADA56193	ADA56193 Human cdn
C 447	18	0.9	511	4	ABs41777	ABs41777 Human l1v	C 520	18	0.9	1014	10	ADA56193	ADA56193 Human cdn
C 448	18	0.9	511	4	ABs39779	ABs39779 Human l1v	C 521	18	0.9	1014	10	ADA56193	ADA56193 Human cdn
C 449	18	0.9	511	5	AAI06680	AAI06680 Probe #66	C 522	18	0.9	1014	10	ADA56193	ADA56193 Human cdn
C 450	18	0.9	511	5	AAI08599	AAI08599 Probe #85	C 523	18	0.9	1014	10	ADA56193	ADA56193 Human cdn
C 451	18	0.9	511	6	ABs16216	ABs16216 Human gen	C 524	18	0.9	1014	10	ADA56193	ADA56193 Human cdn
C 452	18	0.9	511	6	ABs16216	ABs16216 Human gen	C 525	18	0.9	1014	10	ADA56193	ADA56193 Human cdn
C 453	18	0.9	511	6	ABs16216	ABs16216 Human gen	C 526	18	0.9	1014	10	ADA56193	ADA56193 Human cdn
C 454	18	0.9	511	6	ABs16216	ABs16216 Human gen	C 527	18	0.9	1014	10	ADA56193	ADA56193 Human cdn
C 455	18	0.9	511	6	ABs16216	ABs16216 Human gen	C 528	18	0.9	1014	10	ADA56193	ADA56193 Human cdn
C 456	18	0.9	511	6	ABs16216	ABs16216 Human gen	C 529	18	0.9	1014	10	ADA56193	ADA56193 Human cdn
C 457	18	0.9	511	6	ABs16216	ABs16216 Human gen	C 530	18	0.9	1014	10	ADA56193	ADA56193 Human cdn
C 458	18	0.9	511	6	ABs16216	ABs16216 Human gen	C 531	18	0.9	1014	10	ADA56193	ADA56193 Human cdn
C 459	18	0.9	511	6	ABs16216	ABs16216 Human gen	C 532	18	0.9	1014	10	ADA56193	ADA56193 Human cdn

533	18	0.9	1215	6	AB052839	Abq52839 Oligonucle	C 606	18	0.9	2431	6	ABN95768	Abn95768 Gene #226
534	18	0.9	1239	3	AA046261	Aac46261 Arabidops	C 607	18	0.9	2431	11	ADJ13872	Adj13872 Human cDN
535	18	0.9	1239	3	AA032853	Aac32853 Arabidops	C 608	18	0.9	2431	8	ADA70969	Ada70969 Rice gene
536	18	0.9	1272	3	ADA48527	Ada48527 Rice gene	C 609	18	0.9	2453	4	ABL22256	AbL22256 Drosophill
537	18	0.9	1276	3	AA15086	Aa15086 Transcript	C 610	18	0.9	2454	4	AAH77922	Aah77922 Nucleotid
538	18	0.9	1295	8	ACA32245	Ac32245 Prokaryot	C 611	18	0.9	2505	8	AB223069	Ab223069 Human GPC
539	18	0.9	1321	12	AD67449	Ad67449 Human ova	C 612	18	0.9	2559	12	AD002358	Ad002358 Thalecres
540	18	0.9	1360	1	AAAN90702	Aan90702 Rpt-1 cto	C 613	18	0.9	2564	4	ABL21816	AbL21816 Drosophill
541	18	0.9	1376	4	AA508155	Aas08155 Mammalian	C 614	18	0.9	2599	5	AB14651	Ab14651 Human ner
542	18	0.9	1390	2	AAV84524	Aav84524 Human sec	C 615	18	0.9	2610	10	ADD5878	Add5878 Thalecres
543	18	0.9	1390	4	ABAB3307	Abab3307 Human sec	C 616	18	0.9	2633	5	ABA20784	AbA20784 Human Cen
544	18	0.9	1390	4	ACH04808	Ach04808 Novel hum	C 617	18	0.9	2633	12	ADN41798	Adn41798 Novel hum
545	18	0.9	1390	3	ACD44618	Acd44618 Human cDN	C 618	18	0.9	2633	12	AAQ39212	Aaq39212 CNP-B CD
546	18	0.9	1392	3	ACS05457	Acs05457 Arabidops	C 619	18	0.9	2682	9	ACA62959	AcA62959 DNA encod
547	18	0.9	1393	2	ADB69365	Ad69365 C. neofor	C 620	18	0.9	2738	4	AB108506	Ab108506 Drosophill
548	18	0.9	1420	4	AB1070103	Ab1070103 Malarial	C 621	18	0.9	2826	3	AA098975	Aa098975 Human pan
549	18	0.9	1420	4	AB110201	Ab110201 Drosophill	C 622	18	0.9	2826	6	AB232643	Ab232643 Candida a
550	18	0.9	1428	3	AAA99465	Aaa99465 Sakuranet	C 623	18	0.9	2829	10	AD036061	Ad036061 C. neofor
551	18	0.9	1452	10	ACC61055	Acc61055 Gene sequ	C 624	18	0.9	3041	12	ADO36061	Ado36061 Novel mou
552	18	0.9	1452	10	ADK62761	Adk62761 Disease t	C 625	18	0.9	3098	4	ABL06272	AbL06272 Drosophill
553	18	0.9	1467	3	AAA99468	Aaa99468 Sakuranet	C 626	18	0.9	3240	4	AAH14453	Aah14453 Human cDN
554	18	0.9	1473	12	ADK71738	Adk71738 Rice RNA-	C 627	18	0.9	3283	4	AAK94567	Aak94567 Human ful
555	18	0.9	1494	8	ADA70445	Ada70445 Rice gene	C 628	18	0.9	3417	4	AAK94567	Aak94567 Human ful
556	18	0.9	1497	4	AAFR84402	Aafr84402 Maize BxI	C 629	18	0.9	3417	12	ADL33446	Adl33446 Full leng
557	18	0.9	1508	2	AAV07665	Aav07665 Arabidops	C 630	18	0.9	3417	12	ADL33446	Adl33446 Full leng
558	18	0.9	1508	2	AAV07665	Aav07665 Arabidops	C 631	18	0.9	3419	12	ADQ22081	Adq22081 Human sof
559	18	0.9	1513	3	AA039552	Aa039552 Arabidops	C 632	18	0.9	3420	4	ABL10200	AbL10200 Drosophill
560	18	0.9	1544	4	ABE09206	AbE09206 Human slo	C 633	18	0.9	3615	3	AAA64660	Aaa64660 DNA encod
561	18	0.9	1544	4	AAK52671	Aak52671 Human pol	C 634	18	0.9	3729	5	AAH81775	Aah81775 Human dif
562	18	0.9	1554	6	AB232587	Ab232587 Candida a	C 635	18	0.9	3765	5	AAH81775	Aah81775 Human dif
563	18	0.9	1601	3	AA038735	Aa038735 Arabidops	C 636	18	0.9	3787	5	AAH81775	Aah81775 Human dif
564	18	0.9	1602	3	AA038735	Aa038735 Arabidops	C 637	18	0.9	3787	5	AAH81775	Aah81775 Human dif
565	18	0.9	1677	10	ACC61290	Acc61290 Gene sequ	C 638	18	0.9	3982	12	ADJ67450	Adj67450 Human ova
566	18	0.9	1677	10	ADK63665	Adk63665 Disease t	C 639	18	0.9	4055	12	ADJ67451	Adj67451 Human ova
567	18	0.9	1684	4	AA137453	Aa137453 Human mus	C 640	18	0.9	4114	4	ABL02938	AbL02938 Drosophill
568	18	0.9	1684	4	ABX60441	Abx60441 CDNA enc	C 641	18	0.9	4114	4	ABL18842	AbL18842 Drosophill
569	18	0.9	1684	12	ADJ31191	Adj31191 Human mus	C 642	18	0.9	4257	12	ADU67448	AdU67448 Human ova
570	18	0.9	1734	3	AAH13812	Aah13812 Human cDN	C 643	18	0.9	4371	3	AAA99469	Aaa99469 Human ova
571	18	0.9	1743	3	AA042683	Aa042683 Arabidops	C 644	18	0.9	4371	12	ADH22292	Adh22292 Rice PONG
572	18	0.9	1800	11	ADP64939	Adp64939 Human cen	C 645	18	0.9	4466	2	AAQ70102	Aaq70102 Malarial
573	18	0.9	1800	11	ADP64937	Adp64937 Human cen	C 646	18	0.9	5124	4	ABL19435	AbL19435 Drosophill
574	18	0.9	1806	5	AA66443	Aa66443 DNA encod	C 647	18	0.9	5124	4	ABL19435	AbL19435 Drosophill
575	18	0.9	1812	10	ACF36554	Acf36554 O. sativa	C 648	18	0.9	5241	3	AAA99467	Aaa99467 Sakuranet
576	18	0.9	1832	12	AD126112	Ad126112 Human cDN	C 649	18	0.9	5241	3	AAA99467	Aaa99467 Sakuranet
577	18	0.9	1840	5	ABA20783	AbA20783 Human ner	C 650	18	0.9	5677	12	ADN04071	Adn04071 Human bre
578	18	0.9	1840	5	ADNA71799	Adna71799 Rice gene	C 651	18	0.9	5677	12	ADN04071	Adn04071 Human bre
579	18	0.9	1872	8	ADA71079	Ada71079 Arabidops	C 652	18	0.9	5688	12	ADU67447	AdU67447 Human ova
580	18	0.9	1878	6	AB213608	Ab213608 Arabidops	C 653	18	0.9	5688	12	ADU67447	AdU67447 Human ova
581	18	0.9	1878	6	ADG87846	Adg87846 A. thalia	C 654	18	0.9	5734	10	ADC85382	Adc85382 Human PTP
582	18	0.9	1952	4	AAH29727	Aah29727 S. cerevis	C 655	18	0.9	5797	9	ADA20300	Ada20300 Human ATP
583	18	0.9	1952	4	AAH29727	Aah29727 S. cerevis	C 656	18	0.9	5797	9	ADA20300	Ada20300 Human ATP
584	18	0.9	1962	6	ABZ14737	Abz14737 Arabidops	C 657	18	0.9	6471	4	ABL02797	AbL02797 Drosophill
585	18	0.9	1962	6	ABZ14737	Abz14737 Arabidops	C 658	18	0.9	6471	4	ABL02797	AbL02797 Drosophill
586	18	0.9	1986	11	ADM01444	Adm01444 Human cDN	C 659	18	0.9	7084	8	ACC43645	Aac43645 Nucleotid
587	18	0.9	2000	6	AB216299	Ab216299 Arabidops	C 660	18	0.9	7101	4	ABL28056	AbL28056 Drosophill
588	18	0.9	2000	6	ADA69271	Ada69271 Arabidops	C 661	18	0.9	7172	4	AA859026	Aa859026 DNA encod
589	18	0.9	2038	6	ABN95604	Abn95604 Gene #210	C 662	18	0.9	7263	5	AAI58179	Aai58179 Human pol
590	18	0.9	2067	12	ADM47636	Adm47636 Polynucle	C 663	18	0.9	7263	5	AAI58179	Aai58179 Human pol
591	18	0.9	2071	1	AAAN90960	Aaan90960 Promoter	C 664	18	0.9	7263	5	AAI58179	Aai58179 Human pol
592	18	0.9	2090	12	ADP22429	Adp22429 Sea-sequi	C 665	18	0.9	7326	3	AAA70095	Aaa70095 Plasmidnu
593	18	0.9	2093	4	AA159106	Aa159106 Human pol	C 666	18	0.9	7326	3	AAA70095	Aaa70095 Plasmidnu
594	18	0.9	2093	5	AD099329	Ad099329 DNA encod	C 667	18	0.9	7599	11	ADM29297	Adm29297 Human nov
595	18	0.9	2093	5	ADB49089	Adb49089 Novel hum	C 668	18	0.9	7665	11	ADM29297	Adm29297 Human nov
596	18	0.9	2102	10	ADB63120	Adb63120 Human cDN	C 669	18	0.9	7726	4	ABL07924	AbL07924 Drosophill
597	18	0.9	2124	4	AA054915	Aa054915 Nucleotid	C 670	18	0.9	7726	4	ABL07924	AbL07924 Drosophill
598	18	0.9	2135	3	AAA57881	Aaa57881 Arabidops	C 671	18	0.9	7791	2	AA084660	Aa084660 Human cal
599	18	0.9	2159	2	AAV07667	Aav07667 Maize DIM	C 672	18	0.9	7791	6	AA084660	Aa084660 Human cal
600	18	0.9	2169	10	AD157346	Ad157346 Human PYR	C 673	18	0.9	7791	12	ADJ38340	Adj38340 Human cal
601	18	0.9	2195	3	ABL23278	AbL23278 Drosophill	C 674	18	0.9	7791	12	ADJ38340	Adj38340 Human cal
602	18	0.9	2345	3	AA047265	Aa047265 Arabidops	C 675	18	0.9	7808	2	AA084659	Aa084659 Human neu
603	18	0.9	2355	12	ADQ24169	Adq24169 Human sof	C 676	18	0.9	7808	3	AAA71778	Aaa71778 Human cal
604	18	0.9	2406	4	ABL30485	AbL30485 Drosophill	C 677	18	0.9	7808	3	AAA71778	Aaa71778 Human cal
605	18	0.9	2415	6	ABK98553	Abk98553 BectinHum	C 678	18	0.9	7808	8	AB258368	Ab258368 Human cal

C 679	18	0.9	7808	12	ADJ38338	Human	cal	C 752	17	0.9	46	12	ADH69917
C 680	18	0.9	7808	12	ADM57720	Human	cal	C 753	17	0.9	51	3	AAAT77472
C 681	18	0.9	7812	12	ADP21334	Gene	CACN	C 754	17	0.9	51	3	AAAT77458
C 682	18	0.9	7827	6	ABZ35311	Human	gen	C 755	17	0.9	51	3	AAAT77475
C 683	18	0.9	7847	11	ADM29295	Human	nov	C 756	17	0.9	51	3	AAAT77471
C 684	18	0.9	8307	4	AB123161	Drosophil		C 757	17	0.9	51	3	AAAT77474
C 685	18	0.9	8338	2	AAQ73500	DNA	encod	C 758	17	0.9	51	3	AAAT77470
C 686	18	0.9	9291	4	ABL20426	Drosophil		C 759	17	0.9	51	3	AAAT77469
C 687	18	0.9	9321	12	ADN97063	Human	sup	C 760	17	0.9	60	6	ABN46076
C 688	18	0.9	9522	10	ADQ99110	Human	KP	C 761	17	0.9	65	6	ABZ28921
C 689	18	0.9	10079	2	AAQ88057	Human	EC-	C 762	17	0.9	90	4	AAZ36682
C 690	18	0.9	10079	2	AAQ92317	Human	EC-	C 763	17	0.9	94	3	AAA36682
C 691	18	0.9	10079	3	AAZ28294	Human	sup	C 764	17	0.9	98	12	ACH89206
C 692	18	0.9	10079	10	ADL13925	Osteoearth		C 765	17	0.9	99	12	ACH84145
C 693	18	0.9	10079	11	ADM15669	Human	EC-	C 766	17	0.9	100	8	ACD79044
C 694	18	0.9	10079	12	ADQ005100	DNA	encod	C 767	17	0.9	104	3	AAC24011
C 695	18	0.9	11157	4	ABA82023	Wound	hea	C 768	17	0.9	105	2	AAV55843
C 696	18	0.9	11331	5	AAZ85696	DNA	encod	C 769	17	0.9	107	4	AAH62839
C 697	18	0.9	11597	4	AB123160	Drosophil		C 770	17	0.9	108	4	AAK58644
C 698	18	0.9	12124	2	AAV62854	Cucumber		C 771	17	0.9	117	4	AAI25222
C 699	18	0.9	12124	2	AAV62854	Cucumber		C 772	17	0.9	117	4	ABA71012
C 700	18	0.9	12374	10	ADC86480	Human	GPC	C 773	17	0.9	117	4	AAI51214
C 701	18	0.9	13329	5	AAZ71562	DNA	encod	C 774	17	0.9	117	4	ABA37426
C 702	18	0.9	14770	6	ABL68257	Colon	ade	C 775	17	0.9	117	4	AAK45261
C 703	18	0.9	14770	6	ABL68257	Kidney	ca	C 776	17	0.9	117	4	AAK45261
C 704	18	0.9	14770	6	ABL68257	Kidney	ca	C 777	17	0.9	117	4	AAK45261
C 705	18	0.9	14770	10	ADB31314	Testoster		C 778	17	0.9	117	4	ABSA4936
C 706	18	0.9	14797	5	AAZ65159	DNA	encod	C 779	17	0.9	117	4	ABSA4936
C 707	18	0.9	15187	5	AAZ65159	DNA	encod	C 780	17	0.9	118	4	ABA74515
C 708	18	0.9	15439	4	AAZ16515	Human	end	C 781	17	0.9	118	4	AAI54991
C 709	18	0.9	15439	4	AAZ16515	Human	end	C 782	17	0.9	118	4	AAK49158
C 710	18	0.9	15439	9	ADA27276	Genomic	D	C 783	17	0.9	118	4	AAK22984
C 711	18	0.9	15439	10	ADA12879	Human	DNA	C 784	17	0.9	118	4	AAK22984
C 712	18	0.9	15656	8	AAZ50180	Human	sec	C 785	17	0.9	121	6	ABQ97104
C 713	18	0.9	17073	4	AB119434	Drosophil		C 786	17	0.9	126	10	ACA55

825	17	0.9	157	4	ABA39280	Abp39280 Probe #17	C 898	17	0.9	242	4	ABA48792	Abp48792 Human bre
826	17	0.9	157	4	AAK49004	Aak49004 Human bre	C 899	17	0.9	242	4	ABA37965	Abp37965 Probe #16
827	17	0.9	157	4	AAK22833	Aak22833 Human bre	C 900	17	0.9	242	4	ABA33768	Abp33768 Probe #12
828	17	0.9	157	4	ABSA6665	Abp6665 Human bre	C 901	17	0.9	242	4	AAK6439	Aak6439 Human bre
829	17	0.9	157	6	ABSA22640	Abp22640 Human bre	C 902	17	0.9	242	4	AAK40862	Aak40862 Human bre
830	17	0.9	166	6	ABQ96742	Abq96742 Mouse ES	C 903	17	0.9	242	4	AAK51312	Aak51312 Human bre
831	17	0.9	166	12	ACH93320	ACH93320 Mouse ES	C 904	17	0.9	242	4	AAK20352	Aak20352 Human bre
832	17	0.9	167	6	ABL40825	AbL40825 Human bre	C 905	17	0.9	242	4	ABSA6168	Abp6168 Human bre
833	17	0.9	171	4	ABA72451	AbA72451 Human bre	C 906	17	0.9	242	4	AAK20352	Aak20352 Human bre
834	17	0.9	171	4	AAI52861	AAI52861 Probe #21	C 907	17	0.9	242	4	ABSA60439	Abp60439 Human bre
835	17	0.9	171	4	AAK47055	Aak47055 Human bre	C 908	17	0.9	242	5	AAI07332	AAI07332 Probe #73
836	17	0.9	171	4	AAK20872	Aak20872 Human bre	C 909	17	0.9	242	6	ABSA20764	Abp20764 Human bre
837	17	0.9	172	4	ABSA6787	Abp6787 Human bre	C 910	17	0.9	245	4	ABSA14818	Abp14818 Human bre
838	17	0.9	172	4	AAK55739	Aak55739 Human bre	C 911	17	0.9	245	4	AAI52374	AAI52374 Probe #21
839	17	0.9	174	12	ACH81135	ACH81135 Human bre	C 912	17	0.9	245	4	AAK46521	Aak46521 Human bre
840	17	0.9	179	6	ABQ98122	Abq98122 Mouse ES	C 913	17	0.9	245	4	ABSA6237	Abp6237 Human bre
841	17	0.9	184	4	ABA120994	AbA120994 Probe #10	C 914	17	0.9	245	6	ABSA6278	Abp6278 Human bre
842	17	0.9	184	4	ABA48184	AbA48184 Human bre	C 915	17	0.9	256	10	ABSA20878	Abp20878 Human bre
843	17	0.9	184	4	AAK40228	Aak40228 Human bre	C 916	17	0.9	258	12	ACH81394	ACH81394 Human bre
844	17	0.9	184	4	AAK14486	Aak14486 Human bre	C 917	17	0.9	261	4	ABSA6470	Abp6470 Human bre
845	17	0.9	184	6	ABSA71097	Abp71097 Human bre	C 918	17	0.9	261	4	AAI44840	AAI44840 Probe #13
846	17	0.9	184	10	ADD69033	ADD69033 Human bre	C 919	17	0.9	261	4	ABSA6790	Abp6790 Human bre
847	17	0.9	187	4	AAI24014	AAI24014 Probe #13	C 920	17	0.9	261	4	AAK38836	Aak38836 Human bre
848	17	0.9	187	4	ABSA69127	Abp69127 Human bre	C 921	17	0.9	261	4	AAK13107	Aak13107 Human bre
849	17	0.9	187	4	AAI49312	AAI49312 Probe #17	C 922	17	0.9	261	4	ABSA31794	Abp31794 Human bre
850	17	0.9	187	4	AAK43237	Aak43237 Human bre	C 923	17	0.9	261	4	AAK38836	Aak38836 Human bre
851	17	0.9	187	4	AAK17438	Aak17438 Human bre	C 924	17	0.9	261	4	AAK13107	Aak13107 Human bre
852	17	0.9	187	5	AAI09597	AAI09597 Probe #95	C 925	17	0.9	261	4	ABSA38421	Abp38421 Human bre
853	17	0.9	189	4	AAI25169	AAI25169 Probe #15	C 926	17	0.9	261	5	AAI05363	AAI05363 Probe #53
854	17	0.9	189	4	ABSA70934	Abp70934 Human bre	C 927	17	0.9	261	6	ABSA12917	Abp12917 Human bre
855	17	0.9	189	4	AAI51123	AAI51123 Probe #19	C 928	17	0.9	261	12	ACH86903	ACH86903 Human bre
856	17	0.9	189	4	ABSA73677	Abp73677 Human bre	C 929	17	0.9	264	12	ADP94049	ADP94049 Human bre
857	17	0.9	189	4	AAK45170	Aak45170 Human bre	C 930	17	0.9	270	6	ABSA15934	Abp15934 Human bre
858	17	0.9	189	4	AAK19205	Aak19205 Human bre	C 931	17	0.9	270	6	AAK131893	Aak131893 Human bre
859	17	0.9	189	4	ABSA4842	Abp4842 Human bre	C 932	17	0.9	276	4	AAI720201	AAI720201 Probe #10
860	17	0.9	189	6	ABSA19420	Abp19420 Human bre	C 933	17	0.9	276	4	ABSA65230	Abp65230 Human bre
861	17	0.9	198	4	ABSA72990	Abp72990 Human bre	C 934	17	0.9	276	4	AAI45401	AAI45401 Probe #14
862	17	0.9	198	4	AAI53415	AAI53415 Probe #22	C 935	17	0.9	276	4	ABSA47345	Abp47345 Human bre
863	17	0.9	198	4	AAK47583	Aak47583 Human bre	C 936	17	0.9	276	4	ABSA32331	Abp32331 Human bre
864	17	0.9	198	4	ABSA21422	Abp21422 Human bre	C 937	17	0.9	276	4	AAK39388	Aak39388 Human bre
865	17	0.9	198	4	ABSA7319	Abp7319 Human bre	C 938	17	0.9	276	4	AAK13647	Aak13647 Human bre
866	17	0.9	223	12	ACH84117	ACH84117 Human bre	C 939	17	0.9	276	4	ABSA38976	Abp38976 Human bre
867	17	0.9	223	4	ABSA73861	Abp73861 Human bre	C 940	17	0.9	276	5	AAI05905	AAI05905 Probe #58
868	17	0.9	225	4	AAI54307	AAI54307 Probe #22	C 941	17	0.9	276	6	ABSA13475	Abp13475 Human bre
869	17	0.9	225	4	AAK48479	Aak48479 Human bre	C 942	17	0.9	279	9	AAI18001	AAI18001 Probe #14
870	17	0.9	225	4	AAK22314	Aak22314 Human bre	C 943	17	0.9	280	3	AAK31861	Aak31861 Human bre
871	17	0.9	225	4	ABSA48173	Abp48173 Human bre	C 944	17	0.9	285	3	AAK04394	AAK04394 Human bre
872	17	0.9	232	4	AAI22451	AAI22451 Probe #12	C 945	17	0.9	286	8	ABX48171	ABX48171 Human bre
873	17	0.9	232	4	ABSA67527	Abp67527 Human bre	C 946	17	0.9	292	10	ABX86453	ABX86453 Human bre
874	17	0.9	232	4	AAI47743	AAI47743 Probe #16	C 947	17	0.9	292	5	ABSA7936	Abp7936 Human bre
875	17	0.9	232	4	ABSA49623	Abp49623 Human bre	C 948	17	0.9	295	4	AAI28183	AAI28183 Probe #14
876	17	0.9	232	4	ABSA4608	Abp4608 Human bre	C 949	17	0.9	299	4	ABSA69302	Abp69302 Human bre
877	17	0.9	232	4	AAK41698	Aak41698 Human bre	C 950	17	0.9	299	4	AAI49470	AAI49470 Probe #18
878	17	0.9	232	4	AAK15953	Aak15953 Human bre	C 951	17	0.9	299	4	ABSA51297	Abp51297 Human bre
879	17	0.9	232	4	ABSA41287	Abp41287 Human bre	C 952	17	0.9	299	4	ABSA36233	Abp36233 Human bre
880	17	0.9	232	6	ABSA15705	Abp15705 Human bre	C 953	17	0.9	299	4	AAK43403	Aak43403 Human bre
881	17	0.9	232	5	ABSA15705	Abp15705 Human bre	C 954	17	0.9	299	4	AAK3403	Aak3403 Human bre
882	17	0.9	234	4	AAI21604	AAI21604 Probe #11	C 955	17	0.9	299	4	AAK17588	Aak17588 Human bre
883	17	0.9	234	4	ABSA6681	Abp6681 Human bre	C 956	17	0.9	299	4	ABSA3023	Abp3023 Human bre
884	17	0.9	234	4	ABSA4893	Abp4893 Human bre	C 957	17	0.9	299	4	AAI09746	AAI09746 Probe #97
885	17	0.9	234	4	ABSA4893	Abp4893 Human bre	C 958	17	0.9	299	6	ABSA17496	Abp17496 Human bre
886	17	0.9	234	4	ABSA3741	Abp3741 Human bre	C 959	17	0.9	301	4	AAI19578	AAI19578 Probe #95
887	17	0.9	234	4	AAK10838	Aak10838 Human bre	C 960	17	0.9	301	4	ABSA4601	Abp4601 Human bre
888	17	0.9	234	4	AAK15107	Aak15107 Human bre	C 961	17	0.9	301	4	AAI44771	AAI44771 Probe #13
889	17	0.9	234	4	ABSA40416	Abp40416 Human bre	C 962	17	0.9	301	4	ABSA46774	Abp46774 Human bre
890	17	0.9	234	5	ABSA107299	Abp107299 Probe #72	C 963	17	0.9	301	4	ABSA1727	Abp1727 Human bre
891	17	0.9	234	6	ABSA14789	Abp14789 Human bre	C 964	17	0.9	301	4	AAK38772	AAK38772 Human bre
892	17	0.9	241	12	ADQ21395	ADQ21395 Human bre	C 965	17	0.9	301	4	AAK13041	AAK13041 Human bre
893	17	0.9	242	4	ABSA6709	Abp6709 Human bre	C 966	17	0.9	301	4	ABSA38353	Abp38353 Human bre
894	17	0.9	242	4	ABSA71959	Abp71959 Human bre	C 967	17	0.9	301	5	AAI05298	AAI05298 Probe #52
895	17	0.9	242	4	ABSA71959	Abp71959 Human bre	C 968	17	0.9	301	6	ABSA12847	Abp12847 Human bre
896	17	0.9	242	4	ABSA71959	Abp71959 Human bre	C 969	17	0.9	313	8	ABSA72992	Abp72992 Human bre
897	17	0.9	242	4	ABSA72992	Abp72992 Human bre	C 970	17	0.9	314	4	AAI21241	AAI21241 Probe #11



971 17 0.9 314 4 ABa66321 Human foe  
 972 17 0.9 314 4 Aa146512 Probe #15  
 973 17 0.9 314 4 ABa48424 Human bre  
 974 17 0.9 314 4 ABa33385 Probe #11  
 975 17 0.9 314 4 AaK40481 Human bon  
 976 17 0.9 314 4 AaK14739 Human bra  
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 978 17 0.9 314 5 Aa106950 Probe #69  
 979 17 0.9 314 6 ABs14472 Human gen  
 980 17 0.9 320 11 AD130833 Human CDN  
 981 17 0.9 320 10 ACD96554 Human col  
 982 17 0.9 324 6 ABs71103 Human phy  
 983 17 0.9 324 10 Aa144331 Human pny  
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 985 17 0.9 326 4 Aa119635 Human B8  
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 987 17 0.9 326 4 Aa144831 Probe #13  
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 989 17 0.9 326 4 ABa31785 Probe #10  
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 993 17 0.9 326 4 Aa105354 Probe #53  
 994 17 0.9 326 5 ABs12908 Human gen  
 995 17 0.9 331 5 AaM19246 Novel hum  
 996 17 0.9 333 12 ACh80520 Human gen  
 997 17 0.9 334 3 AaC76758 Human ORF  
 998 17 0.9 336 6 ABq86023 Arabidops  
 999 17 0.9 337 3 AaF09102 Fusaarium  
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## ALIGNMENTS

## RESULT 1

AAf77094 standard; DNA; 1944 BP.

AAf77094;

17-MAY-2001 (first entry)

Brassica napus PERK1 DNA.

Proline-rich extensin-like receptor kinase; PERK; resistance; plant; ds.

Brassica napus.

W0200114563-A1.

01-MAR-2001.

18-AUG-2000; 2000MO-CA000966.

19-AUG-1999; 99US-0149466P.

13-OCT-1999; 99US-0159122P.

(GORI/) GORING D.

(SILV/) SILVA N.

Goring D, Silva N;

WPI; 2001-244305/25.

New proline-rich, extensin-like receptor kinase nucleic acids and

polypeptides useful for increasing plant wounding or pathogen resistance,

or for producing transgenic plants with increased wounding or pathogen

resistance.

Claim 6; Fig 1; 91pp; English.

The present invention relates to proline-rich extensin-like receptor

CC kinase (PERK). The PERK nucleic acids and polypeptides are useful for  
 CC increasing the resistance of plants to wounding and pathogens. These are  
 CC also useful for producing transgenic plants with increased wounding and  
 CC pathogen resistance compared with a wild type plant, as well as in assays  
 CC for identifying and developing compounds to inhibit and/or enhance  
 CC polypeptide function directly

SQ Sequence 1944 BP; 464 A; 550 C; 459 G; 471 T; 0 U; 0 Other;

Query Match 100.0%; Score 1944; DB 4; Length 1944;

Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;

Matches 1944; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ATGTCCTCGGCGCGCTCTCGGAGTGGCTTCCATCTCCATCAAACTCCGACA 60  
 1 ATGTCCTCGGCGCGCTCTCGGAGTGGCTTCCATCTCCATCAAACTCCGACA 60

61 ACCACGACTCTCTCTCGGAGTGGCTTCCATCTCCATCAAACTCCGACA 120  
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121 CCATCCACTATTCGCAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 180  
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181 CCATCTCCACCACTCCATCTCAAGCGGATCTCCACCTCTCTCTCTCTCTCTCT 240  
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241 CCGCTCTCCACCTCCATCTCAAGCGGATCTCCACCTCTCTCTCTCTCTCTCT 300  
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361 CCATCT 420  
 361 CCATCT 420

421 GGAATGCGCATCGGAGAGTGGCTCTGCTGTAAGTGAAGTGAAGTGAAGTGA 480  
 421 GGAATGCGCATCGGAGAGTGGCTCTGCTGTAAGTGAAGTGAAGTGAAGTGA 480

481 AAGAAGAACGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540  
 481 AAGAAGAACGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540

541 GGTCCAAAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600  
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601 ACACCAAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660  
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661 CCACGCAAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720  
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781 AGCATTTTCATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840  
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841 TTAGGCAAGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900  
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QY 901 GCTGTGAAGCAGTTGAAAGTTGGAGTGTGTCAGGAGAGAGAGTTTCAGGAGAGGTT 960
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Db 1081 CATGGCGAGGAGCGGCTCAATGAGAGAGACAGATTGAAGTTGCTCTTGATCT 1140
QY 1141 GCTAAAGACCTTCTTATCTTCATGAAAGTTGCAATCTTAAATCATTCACCGTGATTC 1200
Db 1141 GCTAAAGACCTTCTTATCTTCATGAAAGTTGCAATCTTAAATCATTCACCGTGATTC 1200
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Db 1201 AAGGCTTCAACATATGATGATGATTTCAAGTTGAAGCTTAAGTTGCTGATTTGGTCTT 1260
QY 1261 GCTAAGATTGCTTCTGATACAAACGCAATGATCAACGCTGATGAGGAACCTTTGGG 1320
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QY 1321 TACTTGCTCCGGAATACGCTGCAAGCGGAAAGCTCAGAGAAAGTCTGACGTTTCTCA 1380
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Db 1741 AGCCAGTCAATGAAAGATGAAAGATTTAGAAAATGCGACTTGAAGTCAAGAGTAC 1800
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Db 1801 AACGCCACGGGTGAGTACAGTATATCCGACAGTGAATGAGATGAGATGAGATGAGATGAG 1860
QY 1861 AGCAGCGAGGGCCAAACACACGCGAAATGAGATGAGATGAGATGAGATGAGATGAGATGAG 1920
Db 1861 AGCAGCGAGGGCCAAACACACGCGAAATGAGATGAGATGAGATGAGATGAGATGAGATGAG 1920
QY 1921 GGTATATGAGACCTTCTCTTTAA 1944
Db 1921 GGTATATGAGACCTTCTCTTTAA 1944

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RESULT 2
ACF36548
ID ACF36548 standard; cDNA; 1944 BP.
XX
AC ACF36548;
XX
DT 18-DEC-2003 (first entry)
XX
DE B. napus PERK1 receptor kinase encoding cDNA.
XX
KW PERK1; transgenic; plant; proline-rich extensin-like receptor kinase;
XX wound; pathogen resistance; plant growth; seed production; gene; ss.
XX
OS Brassica napus.
XX
FH Key Location/Qualifiers
FT 1..1944
FT CDS
FT /tag=a
FT /transl_except=(pos: 1332..1334, aa: Phe)
FT /product="PERK1"
FT /note="Proline-rich Extensin-like Receptor Kinase"
PN MO2003072763-A1.
XX
PD 04-SEP-2003.
XX
PF 28-FEB-2003; 2003WO-CA000274.
XX
PR 28-FEB-2002; 2002CA-02373903.
PR 28-FEB-2002; 2002US-00086464.
XX
PA (GORI/) GORING D.
PA (SILV/) SILVA N.
PA (HAFF/) HAFANI Y Z.
PI Goring D, Silva N, Hafani YZ;
XX
DR WPI; 2003-712727/67.
DR P-FSDB; ABR82937.
XX
PT Producing a transgenic plant having an increased plant resistance, plant
PT growth or seed production comprises transforming a plant with a nucleic
PT acid molecule having a Proline-rich Extensin-like Receptor Kinase
PT activity.
XX
PS Claim 3; Fig 1A; 123pp; English.
XX
CC The invention relates to producing a transgenic plant having increased
CC plant height, number of branches, number of seed pods and/or seed
CC production compared to a non-transgenic plant, and/or quicker flowering
CC or later senescence compared to a non-transgenic plant. The method
CC involves transforming a plant with a vector including a Proline-rich
CC Extensin-like Receptor Kinase (PERK) nucleic acid molecule or a nucleic
CC acid molecule having PERK activity. The method, as well as the PERK
CC nucleic acid molecule and polypeptide, are useful in increasing plant
CC resistance to wounding and pathogens and in increasing plant growth and
CC seed production. The nucleic acid molecule and polypeptide may also be
CC used in producing transgenic plants or transgenic host cells. The present
CC sequence represents a cDNA encoding a B. napus PERK1 receptor kinase
CC polypeptide
XX
SQ Sequence 1944 BP; 464 A; 550 C; 459 G; 471 T; 0 U; 0 Other;
XX
Query Match 100.0%; Score 1944; DB 10; Length 1944;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1944; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGTCTCTGCGCGCGTCTCCGAGGAGTGTGCTCATCTCCATCCATCAAACTCCACA 60
Db 1 ATGTCTCTGCGCGCGTCTCCGAGGAGTGTGCTCATCTCCATCCATCAAACTCCACA 60
QY 61 ACCACGACTCTCTCTCCAGCTTCCGCTCTCTCTCCACCAACCTTCTCTCTCGCGCG 120

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Db	61	ACACCACTCTCTCTCCAGTTCCGCTCTCTCTCCACCAACAACCTTCTCTCCGCG	120
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Db	121	CCATTCGACTTATTCGACATCTCTCTCTCTTCTTCTGCGCTTACACCTTCTCTCTCTCT	180
Qy	181	CCATCTTCACCAACTCGATCTTACGGCGGGATCTTCACACCTCTCTCTCTACGGCGTCTCA	240
Db	181	CCATCTTCACCAACTCGATCTTACGGCGGGATCTTCACCTCTCTCTCTCTCAAGCGTCTCA	240
Qy	241	CCGCGTCCAACTACAGCCCGGATCTCCACCCGCACTGTACTCTCTCTCTGAAACCTT	300
Db	241	CCGCGTCCAACTACAGCCCGGATCTTCACCCGCACTGTACTCTCTCTCTGAAACCTT	300
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Qy	361	CCATCTTCTCTCTGCGCGCGTCTCTTCTTCCGACGGTTATTCACAGAGATGATGGTG	420
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Qy	421	GGAAATCGCAATCGAGAGAGTGCCTGCTGTGTGATGACTCTGAATTTGCTCTCTGT	480
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Qy	541	GCTGCCAAAGCCGAGAGACCTTACGGTGTGACAGAGACAAATGGCGGCAACAAACGCA	600
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Qy	661	CCACGGCAACTCTCTCCACTTCCACCAACCGCTTTCATGACAGACAGCGCGCTCCGAC	720
Db	661	CCACGGCAACTCTCTCCACTTCCACCAACCGCTTTCATGACAGACAGCGCGCTCCGAC	720
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Qy	781	AGCACTTTCACATAGAGAGAGTACGTAGACCAACAAATGGTTCTCCGAGGCAACTTG	840
Db	781	AGCACTTTCACATAGAGAGAGTACGTAGACCAACAAATGGTTCTCTCGAGGCAACTTG	840
Qy	841	TTAGACAACAGCGGGTCTCGTTACGTGCACAAAGGTGTGTTGCTAGTGGAAAGAAATT	900
Db	841	TTAGACAACAGCGGGTCTCGTTACGTGCACAAAGGTGTGTTGCTAGTGGAAAGAAATT	900
Qy	901	GCTGTGAAGCAATTGAAAGTTGGAGTGTCTCAGGAGAGAGAGATTTCAGGAGAGATT	960
Db	901	GCTGTGAAGCAATTGAAAGTTGGAGTGTCTCAGGAGAGAGAGATTTCAGGAGAGATT	960
Qy	961	GAGATCATCAGAGAGATTCAACACAGGCACTCGGTGTCTTTGTTGGTATTTGATGGCC	1020
Db	961	GAGATCATCAGAGAGATTCAACACAGGCACTCGGTGTCTTTGTTGGTATTTGATGGCC	1020
Qy	1021	GGTGGCAAAAGATTGTTGTTCTATAGATTGTCTTCTTAAACAACATCTGAGCTTCACTC	1080
Db	1021	GGTGGCAAAAGATTGTTGTTCTATAGATTGTCTTCTTAAACAACATCTGAGCTTCACTC	1080
Qy	1081	CATGGCAGAGGACCGGCTTACAAATGGAATGAGACACCAATTTGAAGATTGCTTTGGATCT	1140
Db	1081	CATGGCAGAGGACCGGCTTACAAATGGAATGAGACACCAATTTGAAGATTGCTTTGGATCT	1140
Qy	1141	GCTAAAGACCTTCTTATCTTATGAAAGTTGCAATCTGAAATATTTCAACCGTGAATTC	1200
Db	1141	GCTAAAGACCTTCTTATCTTATGAAAGTTGCAATCTGAAATATTTCAACCGTGAATTC	1200

Accession	Gene	Protein	Length	Source	Species	Accession	Gene	Protein	Length	Source	Species
QY	1201	AAGGCTTCAAAACATATATGATAGATATTTCAAGTTTGAAGCTTAAGTTCCTATTTTGGCTT	1260			QY	1201	AAGGCTTCAAAACATATATGATAGATATTTCAAGTTTGAAGCTTAAGTTCCTATTTTGGCTT	1260		
Db	1201	AAGGCTTCAAAACATATATGATAGATATTTCAAGTTTGAAGCTTAAGTTCCTATTTTGGCTT	1260			Db	1201	AAGGCTTCAAAACATATATGATAGATATTTCAAGTTTGAAGCTTAAGTTCCTATTTTGGCTT	1260		
QY	1261	GCTTAAGTTGCTCTGTATACAAACACGACATGTATCAACACGTGTGATGGAAACCTTTGGG	1320			QY	1261	GCTTAAGTTGCTCTGTATACAAACACGACATGTATCAACACGTGTGATGGAAACCTTTGGG	1320		
Db	1261	GCTTAAGTTGCTCTGTATACAAACACGACATGTATCAACACGTGTGATGGAAACCTTTGGG	1320			Db	1261	GCTTAAGTTGCTCTGTATACAAACACGACATGTATCAACACGTGTGATGGAAACCTTTGGG	1320		
QY	1321	TACTTGGCTCCGGAAATACGCTGACGGAAGCTCACGGAGAAAGTCTGACGTTTCTCA	1380			QY	1321	TACTTGGCTCCGGAAATACGCTGACGGAAGCTCACGGAGAAAGTCTGACGTTTCTCA	1380		
Db	1321	TACTTGGCTCCGGAAATACGCTGACGGAAGCTCACGGAGAAAGTCTGACGTTTCTCA	1380			Db	1321	TACTTGGCTCCGGAAATACGCTGACGGAAGCTCACGGAGAAAGTCTGACGTTTCTCA	1380		
QY	1381	TTTGGCGCTGTGCTTTTGGAGCTCATTTACTGACACGTGCACCCGTTGATGCCAACATATGTC	1440			QY	1381	TTTGGCGCTGTGCTTTTGGAGCTCATTTACTGACACGTGCACCCGTTGATGCCAACATATGTC	1440		
Db	1381	TTTGGCGCTGTGCTTTTGGAGCTCATTTACTGACACGTGCACCCGTTGATGCCAACATATGTC	1440			Db	1381	TTTGGCGCTGTGCTTTTGGAGCTCATTTACTGACACGTGCACCCGTTGATGCCAACATATGTC	1440		
QY	1441	TATGTATATACACGCTAGTTGACTGGGACGACCCATATGCTTAAACGACATCTGACGAA	1500			QY	1441	TATGTATATACACGCTAGTTGACTGGGACGACCCATATGCTTAAACGACATCTGACGAA	1500		
Db	1441	TATGTATATACACGCTAGTTGACTGGGACGACCCATATGCTTAAACGACATCTGACGAA	1500			Db	1441	TATGTATATACACGCTAGTTGACTGGGACGACCCATATGCTTAAACGACATCTGACGAA	1500		
QY	1501	GGAGACTTTTGAAGGTTTATGCTGATGCAAGATGATATATGGGTATATGACACAGAGGATG	1560			QY	1501	GGAGACTTTTGAAGGTTTATGCTGATGCAAGATGATATATGGGTATATGACACAGAGGATG	1560		
Db	1501	GGAGACTTTTGAAGGTTTATGCTGATGCAAGATGATATATGGGTATATGACACAGAGGATG	1560			Db	1501	GGAGACTTTTGAAGGTTTATGCTGATGCAAGATGATATATGGGTATATGACACAGAGGATG	1560		
QY	1561	GCTGCGATGTGTGCTTGTGCTGGGCGCTTGTTCGGCATTCAGCTGGCCGACAGCTCCG	1620			QY	1561	GCTGCGATGTGTGCTTGTGCTGGGCGCTTGTTCGGCATTCAGCTGGCCGACAGCTCCG	1620		
Db	1561	GCTGCGATGTGTGCTTGTGCTGGGCGCTTGTTCGGCATTCAGCTGGCCGACAGCTCCG	1620			Db	1561	GCTGCGATGTGTGCTTGTGCTGGGCGCTTGTTCGGCATTCAGCTGGCCGACAGCTCCG	1620		
QY	1621	ATGAGCCGATTTGCGCTGCGTTAGAGAGAAATGATCACTGTCCAGTCTTTAAAGAAAGG	1680			QY	1621	ATGAGCCGATTTGCGCTGCGTTAGAGAGAAATGATCACTGTCCAGTCTTTAAAGAAAGG	1680		
Db	1621	ATGAGCCGATTTGCGCTGCGTTAGAGAGAAATGATCACTGTCCAGTCTTTAAAGAAAGG	1680			Db	1621	ATGAGCCGATTTGCGCTGCGTTAGAGAGAAATGATCACTGTCCAGTCTTTAAAGAAAGG	1680		
QY	1681	ATGAGACCAAGTCAAGCAATGTATACAGCTCATACGGAAGAAACCCGATTTATGACTCG	1740			QY	1681	ATGAGACCAAGTCAAGCAATGTATACAGCTCATACGGAAGAAACCCGATTTATGACTCG	1740		
Db	1681	ATGAGACCAAGTCAAGCAATGTATACAGCTCATACGGAAGAAACCCGATTTATGACTCG	1740			Db	1681	ATGAGACCAAGTCAAGCAATGTATACAGCTCATACGGAAGAAACCCGATTTATGACTCG	1740		
QY	1741	AGCCAGTCAATGAAACATGAAAGATTTAGAAAATGSCACTTGGAACTCAAGAGTAC	1800			QY	1741	AGCCAGTCAATGAAACATGAAAGATTTAGAAAATGSCACTTGGAACTCAAGAGTAC	1800		
Db	1741	AGCCAGTCAATGAAACATGAAAGATTTAGAAAATGSCACTTGGAACTCAAGAGTAC	1800			Db	1741	AGCCAGTCAATGAAACATGAAAGATTTAGAAAATGSCACTTGGAACTCAAGAGTAC	1800		
QY	1801	AACGCCACGGGTGAAGTACAGTAATCCGACCACTGATGACTGTAACCCGTCTGTTCA	1860			QY	1801	AACGCCACGGGTGAAGTACAGTAATCCGACCACTGATGACTGTAACCCGTCTGTTCA	1860		
Db	1801	AACGCCACGGGTGAAGTACAGTAATCCGACCACTGATGACTGTAACCCGTCTGTTCA	1860			Db	1801	AACGCCACGGGTGAAGTACAGTAATCCGACCACTGATGACTGTAACCCGTCTGTTCA	1860		
QY	1861	AGCAGCGAGGCGCAAAACCAACACGGGAAATGGAATGGGGAAGATTAGAGAACCGGTACG	1920			QY	1861	AGCAGCGAGGCGCAAAACCAACACGGGAAATGGAATGGGGAAGATTAGAGAACCGGTACG	1920		
Db	1861	AGCAGCGAGGCGCAAAACCAACACGGGAAATGGAATGGGGAAGATTAGAGAACCGGTACG	1920			Db	1861	AGCAGCGAGGCGCAAAACCAACACGGGAAATGGAATGGGGAAGATTAGAGAACCGGTACG	1920		
QY	1921	GGTTATAGGAGCCTTCTCTTAA	1944			QY	1921	GGTTATAGGAGCCTTCTCTTAA	1944		
Db	1921	GGTTATAGGAGCCTTCTCTTAA	1944			Db					





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PR 23-APR-1999; 99US-0130891P.  
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PR 04-MAY-1999; 99US-0132484P.  
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PR 06-MAY-1999; 99US-0132487P.  
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PR 14-MAY-1999; 99US-0134221P.  
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PR 14-OCT-1999; 99US-0159637P.
XX 14-OCT-1999; 99US-0159638P.
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PR 29-OCT-1999; 99US-0162142P.

Query Match      2.4%; Score 47; DB 3; Length 2324;
Best Local Similarity 100.0%; Pred. No. 2.1e-11;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1585 GCTTGTGTTGCCATTGAGCTGCGCCGACGACCTTCGATGAGCAGAT 1631
DB 1700 GCTTGTGTTGCCATTGAGCTGCGCCGACGACCTTCGATGAGCAGAT 1746

RESULT 6
ADK53814
ID ADK53814 standard; DNA; 685 BP.
XX
AC ADK53814;
DT 06-MAY-2004 (first entry)
DE
XX Plant DNA sequence which confers altered metabolic characteristic #1197.
XX altered metabolic characteristic; plant; acid metabolism;
XX alcohol metabolism; fatty acid metabolism;
XX branched fatty acid metabolism; alkaloid metabolism;
XX amino acid metabolism; ester metabolism; glyceride metabolism;
XX phenolic metabolism; carbohydrate metabolism; steroid metabolism;
XX terpene metabolism; isoprenoid metabolism; alkene metabolism;
XX alkyne metabolism; hydrocarbon metabolism; ketone metabolism;
XX quinone metabolism; disease resistance; gene shuffling; sexual PCR; ds.
XX Unidentified.
OS
XX WO2003020936-A1.
XX
XX 13-MAR-2003.
XX
XX 30-AUG-2002; 2002WO-US027884.
XX
XX 31-AUG-2001; 2001US-0316471P.
XX
XX (DOMC ) DOM CHEM CO.
XX (DOMC ) DOM AGROSCIENCES LLC.
XX
XX Weglarz T, Gachotte R, Blakeslee B, McCreary DA, Pell RJ;
XX Orleto JVB, Crosley R, Reddy AS, Shukla V, Larrina I, Miller BA;
XX WPI, 2003-313091/30.
XX
XX Novel genes that confer altered metabolic characteristics in Nicotiana
XX glauca plants, useful for altering the levels of metabolites e.g.
XX acids, fatty acids, amino acids, carbohydrates, hydrocarbons and steroids.
XX

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PS Claim 1; SEQ ID NO 1197; 2576bp; English.
XX
XX The invention comprises DNA sequences which confer an altered metabolic
XX characteristic when they are expressed in a plant. The DNA sequences of
XX the invention are useful for producing plants with an altered metabolic
XX characteristic, such as: altered acid metabolism, alcohol metabolism,
XX fatty acid metabolism, branched fatty acid metabolism, alkaloid or other
XX base metabolism, altered amino acid metabolism, altered ester metabolism,
XX altered glyceride metabolism, altered steroid, oxygenated terpene, or
XX carbohydrate metabolism, altered phenolic metabolism, altered
XX isoprenoid metabolism, alkene or alkyne metabolism, hydrocarbon
XX metabolism, ketone or quinone metabolism. The DNA sequences of the
XX invention may be used to provide disease resistance in a plant and gene
XX shuffling or sexual PCR procedures. The present nucleic acid represents a
XX DNA sequence of the invention.

SO Sequence 685 BP; 181 A; 130 C; 176 G; 197 T; 0 U; 1 Other;

Query Match      1.4%; Score 27; DB 10; Length 685;
Best Local Similarity 100.0%; Pred. No. 0.051;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1377 CTCATTGGCGTTGTCCTTTTGAGCT 1403
DB 461 CTCATTGGCGTTGTCCTTTTGAGCT 487

RESULT 7
ACF36555
ID ACF36555 standard; DNA; 1515 BP.
XX
AC ACF36555;
DT 18-DEC-2003 (first entry)
DE
XX Z. mays PERK protein encoding genomic DNA.
XX PERK1; transgenic; plant; proline-rich extensin-like receptor kinase;
XX wound; pathogen resistance; plant growth; seed production; maize; gene;
XX ds.
XX
XX Zea mays.
XX
XX WO2003072763-A1.
XX
XX 04-SEP-2003.
XX
XX 26-FEB-2003; 2003WO-CA000274.
XX
XX 28-FEB-2002; 2002CA-02373903.
XX
XX 28-FEB-2002; 2002US-0008464.
XX
XX (GORI/) GORING D.
XX (SILV/) SILVA N.
XX (HAF/) HAFANI Y Z.
XX
XX Goring D, Silva N, Hafani YZ;
XX WPI, 2003-712727/67.
XX
XX Producing a transgenic plant having an increased plant resistance, plant
XX growth or seed production comprises transforming a plant with a nucleic
XX acid molecule having a Proline-rich Extensin-like Receptor Kinase
XX activity.
XX
XX Disclosure; Fig 21b; 123bp; English.
XX
XX The invention relates to producing a transgenic plant having increased
XX plant height, number of branches, number of seed pods and/or seed
XX production compared to a non-transgenic plant, and/or quicker flowering
XX or later senescence compared to a non-transgenic plant. The method
XX involves transforming a plant with a vector including a Proline-rich
XX Extensin-like Receptor Kinase (PERK) nucleic acid molecule or a nucleic
XX

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CC acid molecule having PERK activity. The method, as well as the PERK  
 CC nucleic acid molecule and polypeptide, are useful in increasing plant  
 CC resistance to wounding and pathogens and in increasing plant growth and  
 CC seed production. The nucleic acid molecule and polypeptide may also be  
 CC used in producing transgenic plants or transgenic host cells. The present  
 CC sequence represents a Z. mays PERK protein encoding genomic DNA (TIGR  
 CC Accession No. AY108241)  
 XX

XX Sequence 1515 BP; 400 A; 330 C; 381 G; 404 T; 0 U; 0 Other;

## Query Match

Best Local Similarity 1.3%; Score 26; DB 10; Length 1515;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1231 TTGAAGCTAAGTTCGATTTGG 1256

DB 601 TTGAAGCTAAGTTCGATTTGG 626

## RESULT 8

AAF22305\_06/c

Continuation (7 of 11) of AAF22305 from base 600001 (Arabidopsis thaliana chromosome 4 c  
 WP Sequence split into 11 fragments LOCUS AAF22305 Accession Aaf22305

WP	Fragment Name	Begin	End
WP	AAF22305_00	1	110000
WP	AAF22305_01	100001	210000
WP	AAF22305_02	200001	310000
WP	AAF22305_03	300001	410000
WP	AAF22305_04	400001	510000
WP	AAF22305_05	500001	610000
WP	AAF22305_06	600001	710000
WP	AAF22305_07	700001	810000
WP	AAF22305_08	800001	910000
WP	AAF22305_09	900001	1010000
WP	AAF22305_10	1000001	1082138

## Query Match

Best Local Similarity 1.3%; Score 26; DB 3; Length 110000;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1036 CTGTCTATGAGTTGTTCTTAACAA 1061

DB 109643 CTGTCTATGAGTTGTTCTTAACAA 109618

## RESULT 9

AAF22305\_07/c

Continuation (8 of 11) of AAF22305 from base 700001 (Arabidopsis thaliana chromosome 4 c  
 WP Sequence split into 11 fragments LOCUS AAF22305 Accession Aaf22305

WP	Fragment Name	Begin	End
WP	AAF22305_00	1	110000
WP	AAF22305_01	100001	210000
WP	AAF22305_02	200001	310000
WP	AAF22305_03	300001	410000
WP	AAF22305_04	400001	510000
WP	AAF22305_05	500001	610000
WP	AAF22305_06	600001	710000
WP	AAF22305_07	700001	810000
WP	AAF22305_08	800001	910000
WP	AAF22305_09	900001	1010000
WP	AAF22305_10	1000001	1082138

## Query Match

Best Local Similarity 1.3%; Score 26; DB 3; Length 110000;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1036 CTGTCTATGAGTTGTTCTTAACAA 1061

DB 9643 CTGTCTATGAGTTGTTCTTAACAA 9618

## RESULT 10

ADA70853/c

ID ADA70853 standard; DNA; 1389 BP.

XX ADA70853;

AC 20-NOV-2003 (first entry)

DT Rice gene, SEQ ID 4176.

DE Plant; bacterial infection; fungal infection; viral infection; rice;

KW gene; ds.

OS Oryza sativa.

XX WO2003000898-A1.

XX 03-JAN-2003.

XX 22-JUN-2001; 2001WO-IB001105.

XX 22-JUN-2001; 2001WO-IB001105.

XX (SYGN) SYNGENTA PARTICIPATIONS AG.

XX Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;

XX Katagiri F, Quan S, Tao Y, Whitman S, Xie Z, Zhu T, Zou G;

XX WPI; 2003-175290/17.

PT Identifying at least one gene involved in plant resistance or response to  
 PT pathogenic infection for conferring resistance or tolerance to a plant to  
 PT bacterial, fungal or viral infection by determining or detecting plant  
 PT gene expression.

XX Claim 6; SEQ ID NO 4176; 899bp; English.

CC The present invention relates to a method (M1) for identifying genes  
 CC involved in plant resistance or response to pathogenic infection. M1  
 CC comprises identifying a gene whose expression is significantly altered in  
 CC the incompatible interaction of plant gene expression relative to  
 CC expression of the gene in an uninfected plant, in a mutant plant that  
 CC does not express a gene associated with response to pathogenic infection,  
 CC or in a corresponding incompatible or compatible interaction. (M1) is  
 CC useful for conferring resistance to resistance or tolerance to a plant to  
 CC bacterial, fungal or viral infection. The present sequence was used to  
 CC illustrate the invention.

XX Sequence 1389 BP; 412 A; 278 C; 406 G; 293 T; 0 U; 0 Other;

Query Match 1.2%; Score 24; DB 8; Length 1389;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 670 CTTCTCTCACCCTCCACCGCCT 693

DB 115 CTTCTCTCACCCTCCACCGCCT 92

## RESULT 11

ADA27371

ID ADA27371 standard; DNA; 1515 BP.

AC ADA27371;

XX 20-NOV-2003 (first entry)

DE HIV-16 L1 codon optimised DNA sequence SEQ ID NO:1.

XX cell line; American Type Culture Collection PTA-4047; ATCC-4047;

XX baculoviruses; viral recombinant protein; virus-like particle; vaccine;

XX diagnostic reagent; human papillomavirus type 16; HIV-16; DI; gene; ds.

OS Synthetic.

OS Human papillomavirus type 16.

```

XX Key Location/Qualifiers
FH CDS 1..1515
FT /tag= a
FT /product= "HPV-16 L1 protein"
FT /transl_except= (pos:208..210,aa:Tyr)
FT /transl_except= (pos:295..297,aa:Val)
XX WO2003068904-A2.
XX
XX 21-AUG-2003.
XX
XX 14-FEB-2003; 2003WO-US004516.
XX
XX 14-FEB-2002; 2002US-0356113P.
XX 14-FEB-2002; 2002US-0356118P.
XX 14-FEB-2002; 2002US-0356119P.
XX 14-FEB-2002; 2002US-0356123P.
XX 14-FEB-2002; 2002US-0356126P.
XX 14-FEB-2002; 2002US-0356133P.
XX 14-FEB-2002; 2002US-0356135P.
XX 14-FEB-2002; 2002US-0356150P.
XX 14-FEB-2002; 2002US-0356151P.
XX 14-FEB-2002; 2002US-0356152P.
XX 14-FEB-2002; 2002US-0356154P.
XX 14-FEB-2002; 2002US-0356156P.
XX 14-FEB-2002; 2002US-0356157P.
XX 14-FEB-2002; 2002US-0356161P.
XX 14-FEB-2002; 2002US-0356162P.
XX
XX (NOVA-) NOVAVAX INC.
XX
XX Robinson RA;
XX WPI; 2003-646475/61.
XX P-PSDB; ADA27363.
XX
XX New insect cell line designated ATCC PTA-4047, useful for replicating
PT baculoviruses to produce large amounts of recombinant proteins of
PT medical, pharmaceutical and veterinary importance.
XX
XX Claim 10; Fig 1; 63pp; English.
XX
XX The present invention describes a cell line comprising a cell that is a
CC clone, derivative, mutant and/or transfectant of a cell line designated
CC American Type Culture Collection (ATCC) PTA-4047. The cell upon culture
CC grows continuously and retains the identifying characteristics of the
CC cell line designated ATCC-4047. Also described is a process of making a
CC cell line. The insect cell line is useful in replicating baculoviruses,
CC as a host substrate for baculovirus plaque assays, as a source of insect
CC proteins, acts as a depot for cell transfection to produce recombinant
CC baculoviruses, and in expressing viral recombinant proteins and virus-like
CC Extracellular and intracellular viral recombinant proteins and virus-like
CC particles expressed from the cell line are useful as pharmaceutical
CC compositions, vaccines or diagnostic reagents. The present sequence
CC represents a human papillomavirus type 16 (HPV-16) L1 codon optimised
CC sequence, which is used in the exemplification of the present invention.
XX
XX Sequence 1515 BP; 297 A; 632 C; 308 G; 278 T; 0 U; 0 Other;
SQ
XX
XX Query Match 1.2%; Score 24; DB 9; Length 1515;
XX Best Local Similarity 100.0%; Pred. No. 1.3;
XX Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

AC ADA92549;
XX
XX 20-NOV-2003 (first entry)
XX
XX HPV-16 L1 codon optimised DNA sequence SEQ ID NO:1.
XX
XX codon optimised; viral capsid protein; virus-like particle; VLP;
XX antigenic; human papillomavirus infection; virucide; vaccine;
XX gene therapy; human papillomavirus type 16; dysplasia; infection; HPV-16;
XX L1; gene; ds.
XX
XX Synthetic.
XX Human papillomavirus type 16.
XX
XX Key Location/Qualifiers
FH CDS 1..1515
FT /tag= a
FT /product= "codon optimised L1 amino acid sequence"
FT /transl_except= (pos:208..210,aa:Tyr)
FT /transl_except= (pos:295..297,aa:Val)
XX
XX WO2003068933-A2.
XX
XX 21-AUG-2003.
XX
XX 14-FEB-2003; 2003WO-US004480.
XX
XX 14-FEB-2002; 2002US-0356113P.
XX 14-FEB-2002; 2002US-0356118P.
XX 14-FEB-2002; 2002US-0356119P.
XX 14-FEB-2002; 2002US-0356123P.
XX 14-FEB-2002; 2002US-0356126P.
XX 14-FEB-2002; 2002US-0356133P.
XX 14-FEB-2002; 2002US-0356135P.
XX 14-FEB-2002; 2002US-0356150P.
XX 14-FEB-2002; 2002US-0356151P.
XX 14-FEB-2002; 2002US-0356152P.
XX 14-FEB-2002; 2002US-0356154P.
XX 14-FEB-2002; 2002US-0356156P.
XX 14-FEB-2002; 2002US-0356157P.
XX 14-FEB-2002; 2002US-0356161P.
XX 14-FEB-2002; 2002US-0356162P.
XX
XX (NOVA-) NOVAVAX INC.
XX
XX Robinson RA;
XX WPI; 2003-689664/65.
XX P-PSDB; ADA92541.
XX
XX New codon optimized polynucleotide encoding a viral capsid protein that
PT self assembles into a virus-like particle, useful for diagnosing,
PT preventing or treating human papillomavirus infections or associated
PT disorders.
XX
XX Claim 7; Page 113; 123pp; English.
XX
XX The present invention describes a codon optimised polynucleotide encoding
CC a viral capsid protein that self assembles into a virus-like particle
CC (VLP) that exhibits conformational antigenic epitopes capable of raising
CC neutralising antibodies, where the VLP is expressed from a host cell
CC extracellularly. Also described: (1) a vector comprising the above codon
CC optimised polynucleotide operably linked to a eukaryotic or prokaryotic
CC regulatory control element, capable of replication in prokaryotic and/or
CC eukaryotic host; (2) a host cell comprising the vector; (3) a
CC pharmaceutical or vaccine composition for treating, ameliorating or
CC preventing a papillomavirus related disease or disorder, comprising a
CC multiplicity of VLPs that exhibit conformational antigenic epitopes, and
CC a carrier, diluent or adjuvant; (4) a diagnostic kit for detecting a
CC papillomavirus infection, comprising a multiplicity of VLPs that exhibit
CC conformational antigenic epitopes, and a detection agent comprising a
CC detectable label; (5) a method for preparing the above codon optimised
CC polynucleotide, comprising replacing codons that are underutilised in

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insect cells with codons that are utilised at high levels in insect cells, to create an initially-modified nucleotide sequence, and modifying the initially-modified nucleotide sequence by choosing a preferred codon for the initially-modified sequence, where the ratio of GC nucleotide pairs to AT nucleotide pairs in the further-modified nucleotide sequence trends towards about 1:1, where the number of palindromic and stem-loop DNA structures in the further-modified nucleotide sequence is minimised, and where the number of transcription and post-transcription repressor elements are minimised; and (6) methods for treating, ameliorating or preventing a papillomavirus related disease or disorder, or for protecting an individual against a papillomavirus infection, comprising administering to an individual an amount of the composition or vaccine cited above. The VLP has virucide activity and can be used in vaccines and in gene therapy. The composition and methods of the present invention are useful in diagnosing, preventing or treating human papillomavirus infections or associated disorders, such as dysplasia. The present sequence represents an HPV-16 codon optimised L1 nucleotide sequence from the present invention.

Sequence 1515 BP; 297 A; 632 C; 308 G; 278 T; 0 U; 0 Other;

Query Match 1.2%; Score 24; DB 9; Length 1515;

Best Local Similarity 100.0%; Pred. No. 1.3;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

669 ACCTCTCCACCTCCACCCGCC 692  
1471 ACCTCTCCACCTCCACCCGCC 1494

RESULT 13

ID ADA14298 standard; DNA; 1515 BP.

ADA14298;

06-NOV-2003 (first entry)

HPV-16 L1 codon optimised sequence SEQ ID NO:1.

purification; recombinant extracellular virus-like particle; recombinant intracellular virus-like particle; virus-like particle; VLP; virucide; vaccine; gene therapy; human papillomavirus; HPV; infection; dysplasia; HPV-16; L1; codon optimised; gene; ds.

Human papillomavirus type 16.

Key Location/Qualifiers

CDS 1..1515

/\*tag= a

/product= "HPV-16 L1 protein"

/transl\_except= (pos:208..210,aa:Tyr)

/transl\_except= (pos:295..297,aa:Val)

WO2003068993-A1.

21-AUG-2003.

14-FEB-2003; 2003WO-US004474.

14-FEB-2002; 2002US-0356113P.

14-FEB-2002; 2002US-0356118P.

14-FEB-2002; 2002US-0356119P.

14-FEB-2002; 2002US-0356123P.

14-FEB-2002; 2002US-0356126P.

14-FEB-2002; 2002US-0356133P.

14-FEB-2002; 2002US-0356135P.

14-FEB-2002; 2002US-0356150P.

14-FEB-2002; 2002US-0356151P.

14-FEB-2002; 2002US-0356152P.

14-FEB-2002; 2002US-0356154P.

14-FEB-2002; 2002US-0356156P.

14-FEB-2002; 2002US-0356157P.

14-FEB-2002; 2002US-0356161P.  
14-FEB-2002; 2002US-0356162P.  
(NOVA-) NOVAVAX INC.

Robinson RA; Thompson MM;

WPI; 2003-679645/64.  
P-PSDB; ADA14290.

Purifying a recombinant human papillomavirus (HPV) L1, useful for diagnosing, preventing or treating HPV infections, comprises clarifying, concentrating and diafiltering cells containing HPV particles.

Example 4; Fig 1A-C; 111pp; English.

The present invention describes a method for purifying a recombinant extracellular or intracellular virus-like particle (VLP). The method comprises harvesting a cell suspension comprising cells containing a plurality of VLPs to produce a harvested supernatant, optionally disrupting the harvested cells to produce cell lysates containing the VLP, clarifying the harvested supernatant, concentrating the clarified supernatant, diafiltering the concentrated supernatant, and recovering as Sf-9S deposited as American Type Culture Collection (ATCC) PTA-4047; (2) producing the cell line described above; (3) host cells that express one or more recombinant gene products with an enhanced yield; (4) producing a foreign protein in an insect cell; (5) nucleic acid sequences that correspond to and code for human papillomavirus (HPV) polypeptides; and (6) pharmaceutical compositions comprising an amount of the recombinant viral gene products, VLPs, agonists, antagonists, or the active fragment of a viral gene product. The VLPs have virucide activity, and can be used in vaccines and in gene therapy. The method is useful in isolating and purifying expressed viral gene products, including VLPs, in vitro. The gene products or particles may be used in detecting, preventing or treating HPV infections and associated symptoms like dysplasia. The present sequence represents an HPV-16 L1 codon optimised nucleotide sequence, which is given in the exemplification of the present invention.

Sequence 1515 BP; 297 A; 632 C; 308 G; 278 T; 0 U; 0 Other;

Query Match 1.2%; Score 24; DB 9; Length 1515;

Best Local Similarity 100.0%; Pred. No. 1.3;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

669 ACCTCTCCACCTCCACCCGCC 692  
1471 ACCTCTCCACCTCCACCCGCC 1494

RESULT 14

ID AAD58571 standard; DNA; 1515 BP.

AAD58571;

04-DEC-2003 (first entry)

HPV-16 L1 codon optimised DNA.

vaccine; humoral immunity; cell-mediated immunity; gene therapy; HPV; virucide; papillomavirus infection; gene; Human papillomavirus; ds.

Human papillomavirus.

Key Location/Qualifiers

CDS 1..1515

/\*tag= a

/product= "HPV-16 L1 protein"

/transl\_except= (pos:208..210,aa:Tyr)

/transl\_except= (pos:295..297,aa:Val)

/note= "No stop codon"

/partial

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XX  
PN  
PD 21-AUG-2003.  
XX  
PF 14-FEB-2003; 2003WO-US004473.  
XX  
PR 14-FEB-2002; 2002US-0356113P.  
PR 14-FEB-2002; 2002US-0356118P.  
PR 14-FEB-2002; 2002US-0356119P.  
PR 14-FEB-2002; 2002US-0356123P.  
PR 14-FEB-2002; 2002US-0356126P.  
PR 14-FEB-2002; 2002US-0356133P.  
PR 14-FEB-2002; 2002US-0356135P.  
PR 14-FEB-2002; 2002US-0356150P.  
PR 14-FEB-2002; 2002US-0356151P.  
PR 14-FEB-2002; 2002US-0356152P.  
PR 14-FEB-2002; 2002US-0356154P.  
PR 14-FEB-2002; 2002US-0356156P.  
PR 14-FEB-2002; 2002US-0356157P.  
PR 14-FEB-2002; 2002US-0356161P.  
PR 14-FEB-2002; 2002US-0356162P.  
XX  
PA (NOVA-) NOVAVAX INC.  
PI Robinson RA, Cloce V;  
XX  
XX WPI; 2003-689598/65.  
DR P-PSDB; AAE38615.  
DR  
PT New chimeric virus-like particles comprising a recombinant viral capsid  
PT protein encapsulating a recombinant viral protein, useful for inducing  
PT humoral and/or cell-mediated immunity against papillomavirus infection.  
XX  
PS Claim 10; Fig 1A-1C; 126pp; English.  
XX  
CC The present invention relates to chimeric virus-like particle comprising  
CC a recombinant viral capsid protein that encapsulates a recombinant viral  
CC protein during self assembly into a chimeric virus-like particle and  
CC exhibiting conformational antigenic epitopes capable of eliciting  
CC neutralising antibodies. The vaccine comprising the chimeric virus-like  
CC particles are useful for inducing immunity (humoral and/or cell-mediated  
CC immunity) against papillomavirus infection. The invention is also useful  
CC in gene therapy. The present sequence is HPV (human papillomavirus)-16 L1  
CC codon optimised DNA  
XX  
SQ Sequence 1515 BP; 297 A; 632 C; 308 G; 278 T; 0 U; 0 Other;  
XX  
Query Match 1.2%; Score 24; DB 9; Length 1515;  
Best Local Similarity 100.0%; Pred. No. 1.3;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0.  
QY 669 ACCTCCTCACCTCCACCAACGCGC 692  
|||  
Db 1471 ACCTCCTCACCTCCACCAACGCGC 1494  
XX  
RESULT 15  
ACH93299  
ID ACH93299 standard; DNA; 180 BP.  
XX  
XX ACH93299;  
AC  
DT 29-JUL-2004 (first entry)  
XX  
DE Human genome derived single exon probe #26494.  
XX  
XX Human; probe; ss; gene expression; single exon probe; microarray;  
KW alternative splicing event; genomic alteration.  
XX  
OS Homo sapiens.  
XX

```

XX  US2003194704-A1.
XX  16-OCT-2003.
XX  03-APR-2002, 2002US-00029386.
XX  03-APR-2002, 2002US-00029386.
XX  03-APR-2002, 2002US-00029386.
XX  (PENN/) PENN S G.
XX  (RANK/) RANK D R.
XX  (HANZ/) HANZEL D K.
XX  Penn SG, Rank DR, Hanzel DK;
XX  WPI; 2004-119264/12.
XX  DR
XX  PT New human genome-derived single exon nucleic acid probes useful for human
XX  PT gene expression analysis, for identifying or characterizing alternative
XX  PT splicing events, for assessing genomic alterations or as tools for
XX  PT surveying tissues.
XX  PS Claim 1; SEQ ID NO 26494; 80pp; English.
XX  CC The invention relates to a nucleic acid probe for measuring human gene
XX  CC expression, comprising any of the 27,400 fully defined nucleotide
XX  CC sequences in the specification, or their complements or fragments, and
XX  CC encoding at least 8 amino acids of any of the 6888 amino acid sequences
XX  CC fully defined in the specification. The probe is a single exon probe that
XX  CC hybridizes under high stringency conditions to a nucleic acid molecule
XX  CC expressed in human cells or tissues. Also included are a spatially-
XX  CC addressable set of single exon nucleic acid probes for measuring human
XX  CC gene expression (comprising a plurality of single exon nucleic acid
XX  CC probes cited above, where each of the plurality of probes is separately
XX  CC and addressably isolatable or amplifiable from the plurality), a single
XX  CC exon microarray for measuring human gene expression, a method of
XX  CC measuring human gene expression, a vector comprising the single exon
XX  CC probe cited above, an ORF-encoded peptide comprising at least 8
XX  CC contiguous amino acids of any of the above-mentioned amino acid
XX  CC sequences (optionally with conservative amino acid substitutions), an
XX  CC isolated antibody that binds specifically to a peptide cited above,
XX  CC methods of selling and/or licensing single exon probes or microarrays to
XX  CC a customer desiring to measure gene expression, a method of providing
XX  CC human gene expression data by subscription, and a computer-readable
XX  CC storage medium which contains a database having a plurality of records
XX  CC (each record including data on the expression of a single exon probe
XX  CC cited above. The probe, methods and apparatus are useful in gene
XX  CC expression analysis. The probes may be used as tools for surveying
XX  CC tissues to detect the presence of expressed messages that contain their
XX  CC specific exon, or in constructing genome-derived single exon microarrays.
XX  CC In addition, the probes are used in identifying and characterizing
XX  CC alternative splicing events, in detecting and characterizing gross
XX  CC alterations in the genomic locus that includes their exon, in assessing
XX  CC smaller genomic alterations, in pinning the synthesis of nucleic acids,
XX  CC or in expressing the ORF-encoded peptide. The present sequence is a human
XX  CC single exon probe of the invention. Note: The sequence data for this
XX  CC patent did not form part of the printed specification, but was obtained
XX  CC in electronic format directly from USPTO at
XX  CC seqdata.uspto.gov/sequence.html?docid=20030194704
XX  SQ Sequence 180 BP, 61 A, 29 C, 44 G, 46 T, 0 U, 0 Other:
XX
XX  Query Match 1.2%; Score 23; DB 12; Length 180;
XX  Best Local Similarity 100.0%; Pred. No. 4.1;
XX  Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX  1240 AAGGTGCTGATTGGTGTCTTGC 1262
XX  |||||||
XX  29 AAGGTGCTGATTGGTGTCTTGC 51

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OM nucleic - nucleic search, using sw model

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	1944	100.0	13	US-10-086-464-3	Sequence 3, Appl1
3	29	1.5	80393	US-10-086-038-4	Sequence 4, Appl1
4	26	1.3	268	US-09-923-876-5096	Sequence 5096, Ap
5	26	1.3	268	US-09-923-876-5096	Sequence 5096, Ap
6	26	1.3	808	US-10-767-701-5803	Sequence 5803, Ap
7	26	1.3	951	US-10-425-114-1932	Sequence 1932, Ap
8	26	1.3	1011	US-10-425-114-1932	Sequence 1932, Ap
9	26	1.3	1100	US-10-425-114-1932	Sequence 1932, Ap
10	26	1.3	1134	US-10-425-114-1932	Sequence 1932, Ap
11	26	1.3	1500	US-10-425-114-1932	Sequence 1932, Ap
12	26	1.3	1552	US-10-425-114-1932	Sequence 1932, Ap

13	1.3	1724	16	US-10-425-114-2326	Sequence 2326, Ap
14	1.3	2886	18	US-10-425-115-57011	Sequence 57011, A
15	1.3	6862	18	US-10-425-115-72287	Sequence 72287, A
16	1.3	1101	16	US-10-424-599-122411	Sequence 122411, A
17	1.2	388	17	US-10-437-963-6709	Sequence 6709, Ap
18	1.2	1515	15	US-10-367-095-1	Sequence 1, Appl1
19	1.2	1515	16	US-10-368-046-1	Sequence 1, Appl1
20	1.2	1515	16	US-10-367-367-1	Sequence 1, Appl1
21	1.2	180	15	US-10-029-386-26494	Sequence 26494, A
22	1.2	579	15	US-10-029-386-26494	Sequence 26494, A
23	1.2	1281	16	US-10-106-938A-12	Sequence 12794, A
24	1.2	672	17	US-10-767-795-2653	Sequence 2653, Ap
25	1.2	897	16	US-10-106-938A-11	Sequence 10, Appl1
26	1.2	897	16	US-10-106-938A-11	Sequence 11, Appl1
27	1.2	1281	16	US-10-106-938A-12	Sequence 12, Appl1
28	1.2	1289	15	US-10-378-393-21	Sequence 21, Appl1
29	1.2	1896	17	US-10-437-963-59942	Sequence 59942, A
30	1.2	1939	16	US-10-424-599-1237	Sequence 1237, Ap
31	1.2	1987	15	US-10-378-393-17	Sequence 17, Appl1
32	1.2	4517	23	US-10-093-463-117	Sequence 117, Ap
33	1.2	4586	10	US-09-983-000A-11	GENERAL INFORMATI
34	1.2	4586	15	US-10-102-524-1707	Sequence 1707, Ap
35	1.2	4586	17	US-10-304-019-4	Sequence 4, Appl1
36	1.2	4620	16	US-10-106-938A-11	Sequence 11, Appl1
37	1.2	4620	17	US-10-304-019-11	Sequence 11, Appl1
38	1.2	4620	17	US-10-648-593-52	Sequence 52, Appl1
39	1.2	4626	17	US-10-620-052A-11	Sequence 11, Appl1
40	1.2	4726	13	US-10-087-192-123	Sequence 32, Ap
41	1.2	125974	17	US-10-304-019-12	Sequence 12, Appl1
42	1.2	144035	13	US-10-087-192-322	Sequence 32, Ap
43	1.1	403	18	US-10-425-115-78725	Sequence 78725, A
44	1.1	1776	18	US-10-425-115-136124	Sequence 136124, A
45	1.1	3789	17	US-10-437-963-69323	Sequence 69323, A
46	1.1	169	18	US-10-425-115-92960	Sequence 92960, A
47	1.1	378	17	US-10-767-701-26471	Sequence 26471, A
48	1.1	457	17	US-10-767-701-25071	Sequence 25071, A
49	1.1	512	18	US-10-425-115-65466	Sequence 65466, A
50	1.1	1179	17	US-10-021-323-10099	Sequence 10099, A
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53	1.1	1166	17	US-10-437-963-53026	Sequence 53026, A
54	1.1	1713	18	US-10-425-115-140842	Sequence 140842, A
55	1.1	1797	18	US-10-425-115-174795	Sequence 174795, A
56	1.1	2196	13	US-10-086-464-7	Sequence 7, Appl1
57	1.1	2231	13	US-10-086-464-6	Sequence 6, Appl1
58	1.1	2886	17	US-10-437-963-70177	Sequence 70177, A
59	1.1	82990	15	US-10-292-798-1393	Sequence 1393, Ap
60	1.0	213	9	US-09-867-701-9615	Sequence 9615, Ap
61	1.0	260	16	US-10-424-599-58928	Sequence 58928, A
62	1.0	421	17	US-10-767-701-5416	Sequence 5416, Ap
63	1.0	432	9	US-09-770-423-1122	Sequence 122, Ap
64	1.0	501	17	US-10-437-963-10450	Sequence 10450, A
65	1.0	579	17	US-10-437-963-96775	Sequence 96775, A
66	1.0	609	9	US-09-800-729-55	Sequence 55, Appl1
67	1.0	623	16	US-10-425-114-4896	Sequence 4896, Ap
68	1.0	655	16	US-10-425-114-11463	Sequence 11463, A
69	1.0	678	17	US-10-767-701-1124	Sequence 1124, Ap
70	1.0	687	18	US-10-425-115-4643	Sequence 4643, Ap
71	1.0	727	16	US-10-374-780A-482	Sequence 482, Ap
72	1.0	727	16	US-10-412-6999-993	Sequence 993, Ap
73	1.0	751	16	US-10-425-114-4607	Sequence 4607, Ap
74	1.0	767	16	US-10-412-6999-995	Sequence 995, Ap
75	1.0	823	18	US-10-425-115-49730	Sequence 49730, A
76	1.0	838	17	US-10-425-115-49730	Sequence 49730, A
77	1.0	849	17	US-10-767-701-10055	Sequence 35074, A
78	1.0	918	16	US-10-424-599-54382	Sequence 10055, A
79	1.0	930	15	US-10-156-761-4577	Sequence 4577, Ap
80	1.0	938	16	US-10-403-571-7	Sequence 7, Appl1
81	1.0	990	17	US-10-437-963-74637	Sequence 74637, A
82	1.0	990	17	US-10-077-584-5	Sequence 5, Appl1
83	1.0	1101	14	US-10-437-963-72332	Sequence 72332, A
84	1.0	1101	17	US-10-437-963-72332	Sequence 72332, A
85	1.0	1159	16	US-10-424-599-59138	Sequence 59138, A

86	20	1.0	1182	17	US-10-437-963-64920	Sequence 64920, A	159	19	1.0	268	11	US-09-733-627A-4608	Sequence 4608, App
87	20	1.0	1236	14	US-10-077-584-3	Sequence 3	159	19	1.0	274	18	US-10-425-115-61590	Sequence 61590, A
88	20	1.0	1260	17	US-10-437-963-86081	Sequence 86081, A	160	19	1.0	323	10	US-09-764-872-92	Sequence 92, App
89	20	1.0	1368	18	US-10-739-930-1905	Sequence 1905, App	161	19	1.0	358	9	US-09-810-936-168	Sequence 168, App
90	20	1.0	1373	17	US-10-437-963-55754	Sequence 55754, A	162	19	1.0	358	9	US-09-429-755-168	Sequence 168, App
91	20	1.0	1536	17	US-10-437-963-4006	Sequence 4006, App	163	19	1.0	358	9	US-09-924-400-168	Sequence 168, App
92	20	1.0	1602	17	US-10-437-963-86675	Sequence 86675, A	164	19	1.0	358	9	US-10-212-679-168	Sequence 168, App
93	20	1.0	1617	17	US-10-437-963-94188	Sequence 94188, A	165	19	1.0	358	15	US-10-079-137B-168	Sequence 168, App
94	20	1.0	1687	15	US-10-163-198-40	Sequence 40, App	166	19	1.0	358	16	US-10-437-963-77743	Sequence 77743, A
95	20	1.0	1701	10	US-09-814-353-19123	Sequence 10, App	167	19	1.0	390	17	US-10-425-115-62860	Sequence 62860, A
96	20	1.0	1902	13	US-10-086-464-10	Sequence 61529, A	168	19	1.0	410	18	US-10-425-115-62860	Sequence 62860, A
97	20	1.0	1939	17	US-10-437-963-61529	Sequence 9, App	169	19	1.0	411	17	US-10-437-963-71834	Sequence 71834, A
98	20	1.0	1939	13	US-10-086-464-9	Sequence 2217, App	170	19	1.0	414	17	US-10-437-963-1558	Sequence 1558, App
99	20	1.0	1948	16	US-10-425-114-32217	Sequence 32217, App	171	19	1.0	423	9	US-09-960-352-7506	Sequence 7506, App
100	20	1.0	2120	16	US-10-425-114-35672	Sequence 35672, App	172	19	1.0	430	17	US-10-437-963-100130	Sequence 100130, App
101	20	1.0	2140	18	US-10-425-115-53736	Sequence 53736, A	173	19	1.0	447	17	US-10-437-963-61225	Sequence 61225, A
102	20	1.0	2184	15	US-10-304-946-7	Sequence 7, App	174	19	1.0	449	16	US-10-424-599-10879	Sequence 10879, App
103	20	1.0	2185	18	US-10-739-930-726	Sequence 726, App	175	19	1.0	455	17	US-10-767-701-29553	Sequence 29553, A
104	20	1.0	2227	15	US-10-304-946-5	Sequence 5, App	176	19	1.0	458	17	US-10-437-963-3998	Sequence 3998, App
105	20	1.0	2242	15	US-10-304-946-6	Sequence 6, App	177	19	1.0	459	17	US-10-437-963-3480	Sequence 3480, App
106	20	1.0	2250	17	US-10-437-963-69331	Sequence 69331, A	178	19	1.0	459	17	US-10-437-963-49338	Sequence 49338, A
107	20	1.0	2241	15	US-10-304-946-8	Sequence 8, App	179	19	1.0	463	9	US-09-864-761-5509	Sequence 5509, App
108	20	1.0	2443	17	US-10-437-963-101060	Sequence 101060, A	180	19	1.0	465	10	US-09-918-995-25442	Sequence 25442, A
109	20	1.0	2499	17	US-10-437-963-788	Sequence 788, App	181	19	1.0	484	17	US-10-437-963-57511	Sequence 57511, A
110	20	1.0	2553	17	US-10-437-963-69293	Sequence 69293, A	182	19	1.0	486	16	US-10-424-599-15007	Sequence 15007, A
111	20	1.0	2607	17	US-10-437-963-69298	Sequence 69298, A	183	19	1.0	494	10	US-09-918-995-23336	Sequence 23336, A
112	20	1.0	2621	15	US-10-128-714-159	Sequence 159, App	184	19	1.0	495	16	US-10-424-599-11402	Sequence 11402, A
113	20	1.0	2621	15	US-10-128-714-5159	Sequence 5159, App	185	19	1.0	510	18	US-10-425-115-52035	Sequence 52035, A
114	20	1.0	2653	17	US-10-437-963-69336	Sequence 69336, A	186	19	1.0	511	16	US-10-424-599-94642	Sequence 94642, A
115	20	1.0	2853	17	US-10-437-963-69296	Sequence 69296, A	187	19	1.0	533	15	US-10-029-386-1253	Sequence 1253, A
116	20	1.0	2880	16	US-10-425-114-33031	Sequence 33031, A	188	19	1.0	533	15	US-10-029-386-12953	Sequence 12953, A
117	20	1.0	2881	16	US-10-425-114-33031	Sequence 33031, A	189	19	1.0	565	13	US-10-027-632-5066	Sequence 5066, App
118	20	1.0	2930	17	US-10-425-115-28209	Sequence 28209, A	190	19	1.0	565	13	US-10-027-632-5067	Sequence 5067, App
119	20	1.0	3027	17	US-10-437-963-69291	Sequence 69291, A	191	19	1.0	565	13	US-10-027-632-5067	Sequence 5066, App
120	20	1.0	3046	15	US-10-104-047-1149	Sequence 1149, App	192	19	1.0	565	15	US-10-027-632-5066	Sequence 5066, App
121	20	1.0	3097	14	US-10-101-664A-11	Sequence 11, App	193	19	1.0	565	15	US-10-027-632-5066	Sequence 5067, App
122	20	1.0	3324	17	US-10-437-963-69380	Sequence 69380, A	194	19	1.0	565	15	US-10-027-632-5067	Sequence 664, App
123	20	1.0	4017	17	US-10-437-963-69319	Sequence 69319, A	195	19	1.0	575	13	US-10-027-632-32289	Sequence 32289, App
124	20	1.0	4080	17	US-10-437-963-69319	Sequence 69319, A	196	19	1.0	586	13	US-10-027-632-32290	Sequence 32290, App
125	20	1.0	4248	17	US-10-437-963-88502	Sequence 88502, A	197	19	1.0	586	13	US-10-027-632-32289	Sequence 32289, App
126	20	1.0	4347	17	US-10-437-963-69312	Sequence 69312, A	198	19	1.0	586	15	US-10-027-632-32289	Sequence 32289, App
127	20	1.0	4644	17	US-10-437-963-85119	Sequence 85119, A	199	19	1.0	586	15	US-10-027-632-32290	Sequence 32290, App
128	20	1.0	4674	17	US-10-437-963-92629	Sequence 92629, A	200	19	1.0	597	18	US-10-425-115-25320	Sequence 25320, A
129	20	1.0	4883	17	US-10-437-963-92608	Sequence 92608, A	201	19	1.0	606	17	US-10-425-115-25320	Sequence 25320, A
130	20	1.0	4934	17	US-10-437-963-4830	Sequence 4830, App	202	19	1.0	626	17	US-10-767-701-26059	Sequence 26059, A
131	20	1.0	4960	17	US-10-437-963-8512	Sequence 8512, A	203	19	1.0	629	17	US-09-764-872-677	Sequence 677, App
132	20	1.0	5145	17	US-10-437-963-3509	Sequence 3509, App	204	19	1.0	635	16	US-10-260-238-1578	Sequence 1578, App
133	20	1.0	5157	9	US-09-764-877-2605	Sequence 2605, App	205	19	1.0	638	17	US-10-260-238-1578	Sequence 1578, App
134	20	1.0	5157	16	US-10-242-515-2605	Sequence 2605, App	206	19	1.0	643	16	US-10-767-701-5619	Sequence 5619, App
135	20	1.0	5199	16	US-09-764-877-2607	Sequence 2607, App	207	19	1.0	643	16	US-10-767-701-5619	Sequence 18092, A
136	20	1.0	5284	17	US-10-242-515-2607	Sequence 2607, App	208	19	1.0	650	9	US-09-770-149-530	Sequence 530, App
137	20	1.0	5284	17	US-10-437-963-93167	Sequence 93167, A	209	19	1.0	650	16	US-10-424-599-123917	Sequence 123917, App
138	20	1.0	5720	9	US-09-800-729-18	Sequence 18, App	210	19	1.0	682	13	US-10-027-632-26916	Sequence 26916, A
139	20	1.0	5738	17	US-10-437-963-93221	Sequence 93221, A	211	19	1.0	682	13	US-10-027-632-26916	Sequence 26916, A
140	20	1.0	5769	17	US-09-764-853-134	Sequence 134, App	212	19	1.0	682	15	US-10-027-632-26916	Sequence 26916, A
141	20	1.0	5823	17	US-10-437-963-69288	Sequence 69288, A	213	19	1.0	694	16	US-10-027-632-26916	Sequence 106215, A
142	20	1.0	5868	15	US-10-293-504-2	Sequence 2, App	214	19	1.0	694	16	US-10-424-599-106215	Sequence 106215, A
143	20	1.0	6052	17	US-10-437-963-86097	Sequence 86097, A	215	19	1.0	704	16	US-10-425-114-14276	Sequence 14276, A
144	20	1.0	6135	17	US-10-437-963-14011	Sequence 14011, A	216	19	1.0	719	16	US-10-425-114-23786	Sequence 23786, A
145	20	1.0	6182	18	US-10-425-115-61630	Sequence 61630, A	217	19	1.0	728	13	US-10-027-632-44208	Sequence 44208, A
146	20	1.0	6402	17	US-10-437-963-16557	Sequence 16557, A	218	19	1.0	728	13	US-10-027-632-44208	Sequence 44208, A
147	20	1.0	6916	15	US-10-293-504-1	Sequence 1, App	219	19	1.0	728	15	US-10-027-632-44208	Sequence 44208, A
148	20	1.0	6972	17	US-10-437-963-16522	Sequence 16522, A	220	19	1.0	728	15	US-10-027-632-44208	Sequence 44208, A
149	20	1.0	7142	16	US-10-467-042-21	Sequence 21, App	221	19	1.0	743	18	US-10-425-115-448725	Sequence 448725, A
150	20	1.0	7142	16	US-10-467-042-21	Sequence 21, App	222	19	1.0	757	13	US-10-027-632-19434	Sequence 19434, A
151	20	1.0	41100	9	US-09-755-665-46	Sequence 46, App	223	19	1.0	757	13	US-10-027-632-19434	Sequence 19434, A
152	20	1.0	41100	9	US-10-629-248-46	Sequence 46, App	224	19	1.0	792	18	US-10-425-115-83110	Sequence 83110, A
153	20	1.0	87394	18	US-10-810-788A-6	Sequence 6, App	225	19	1.0	817	18	US-10-425-115-83110	Sequence 83110, A
154	20	1.0	109453	17	US-10-388-838-81	Sequence 81, App	226	19	1.0	830	16	US-10-425-115-8518	Sequence 8518, App
155	20	1.0	9025608	15	US-10-156-761-1	Sequence 1, App	227	19	1.0	836	17	US-10-437-963-64836	Sequence 64836, A
156	19	1.0	105	15	US-10-029-386-14368	Sequence 14368, A	228	19	1.0	836	17	US-10-437-963-64836	Sequence 64836, A
157	19	1.0	141	15	US-10-029-386-15226	Sequence 15226, A	229	19	1.0	853	17	US-10-425-115-8525	Sequence 8525, App
158	19	1.0	217	18	US-10-425-115-102419	Sequence 102419, A	230	19	1.0	889	17	US-10-767-701-2738	Sequence 2738, App
159	19	1.0	257	18	US-10-425-115-47774	Sequence 47774, A	231	19	1.0	909	15	US-10-437-963-86233	Sequence 86233, A

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C 234	19	1.0	925	18	US-10-425-115-83113	Sequence 83113, A	C 307	19	1.0	9487	18	US-10-788-792-43	Sequence 43, App1
C 235	19	1.0	938	18	US-10-425-115-18367	Sequence 18367, A	C 308	19	1.0	9567	10	US-09-738-630-58	Sequence 58, App1
C 236	19	1.0	1023	17	US-10-437-963-59357	Sequence 59357, A	C 309	19	1.0	9657	13	US-10-016-768-12	Sequence 12, App1
C 237	19	1.0	1029	17	US-10-437-963-95316	Sequence 95316, A	C 310	19	1.0	9674	13	US-10-016-768-9	Sequence 9, App1
C 238	19	1.0	1056	16	US-10-425-114-23357	Sequence 23357, A	C 311	19	1.0	9757	13	US-10-311-455-94	Sequence 494, App
C 239	19	1.0	1062	18	US-10-425-115-8520	Sequence 8520, App	C 312	19	1.0	16750	15	US-10-221-714A-36	Sequence 36, App1
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C 242	19	1.0	1077	16	US-10-425-114-33789	Sequence 33789, A	C 315	19	1.0	31124	13	US-10-087-192-163	Sequence 463, App
C 243	19	1.0	1185	18	US-10-425-114-33789	Sequence 33789, A	C 316	19	1.0	60452	13	US-10-087-192-1900	Sequence 1900, App
C 244	19	1.0	1185	18	US-10-425-115-8522	Sequence 8522, App	C 317	19	1.0	75976	17	US-10-322-281-229	Sequence 229, App
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C 246	19	1.0	1215	17	US-10-437-963-9639	Sequence 96399, A	C 319	19	1.0	246940	17	US-10-332-696-58	Sequence 58, App1
C 247	19	1.0	1246	17	US-10-437-963-50650	Sequence 50650, A	C 320	19	1.0	430442	18	US-10-417-375-128	Sequence 128, App
C 248	19	1.0	1293	17	US-10-437-963-39781	Sequence 39781, A	C 321	19	1.0	659158	9	US-09-771-208-20	Sequence 20, App1
C 249	19	1.0	1309	17	US-10-437-963-9222	Sequence 9222, App	C 322	19	1.0	18	13	US-10-086-464-25	Sequence 25, App1
C 250	19	1.0	1322	17	US-10-437-963-40685	Sequence 40685, A	C 323	19	0.9	145	9	US-10-481-763-47	Sequence 27, App1
C 251	19	1.0	1365	17	US-10-767-701-15550	Sequence 15550, A	C 324	18	0.9	145	9	US-09-867-701-8952	Sequence 8952, App
C 252	19	1.0	1380	18	US-10-739-930-577	Sequence 577, App	C 325	18	0.9	147	18	US-10-674-124A-14669	Sequence 14669, A
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C 257	19	1.0	1562	15	US-10-369-493-27227	Sequence 27227, A	C 330	18	0.9	203	9	US-09-738-973-480	Sequence 480, App
C 258	19	1.0	1661	17	US-10-437-963-69005	Sequence 69005, A	C 331	18	0.9	203	9	US-09-867-701-9051	Sequence 9051, App
C 259	19	1.0	1715	17	US-10-437-963-87635	Sequence 87635, A	C 332	18	0.9	203	9	US-09-854-133-480	Sequence 480, App
C 260	19	1.0	1971	18	US-10-425-115-133331	Sequence 133331, A	C 333	18	0.9	203	15	US-10-114-649A-480	Sequence 480, App
C 261	19	1.0	2025	13	US-10-086-464-103	Sequence 13323, A	C 334	18	0.9	203	18	US-10-674-124A-5687	Sequence 5687, App
C 262	19	1.0	2095	16	US-10-425-114-30026	Sequence 30026, A	C 335	18	0.9	209	9	US-09-867-701-8665	Sequence 8665, App
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C 264	19	1.0	2107	16	US-10-424-599-129242	Sequence 129242, A	C 337	18	0.9	227	17	US-09-864-761-19728	Sequence 19728, A
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C 267	19	1.0	2256	17	US-10-437-963-16256	Sequence 16256, A	C 340	18	0.9	247	17	US-10-437-963-1179	Sequence 4179, App
C 268	19	1.0	2327	17	US-10-437-963-4440	Sequence 5440, A	C 341	18	0.9	251	17	US-10-437-963-99520	Sequence 72038, A
C 269	19	1.0	2421	16	US-10-623-272-4	Sequence 5440, A	C 342	18	0.9	251	17	US-10-437-963-99520	Sequence 99520, A
C 270	19	1.0	2487	16	US-10-623-272-54	Sequence 5398, App	C 343	18	0.9	262	9	US-09-867-701-8858	Sequence 8858, App
C 271	19	1.0	2603	15	US-10-094-749-753	Sequence 5387, App	C 344	18	0.9	266	18	US-10-425-115-143302	Sequence 143302, A
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C 273	19	1.0	2850	17	US-10-437-963-5398	Sequence 5398, App	C 346	18	0.9	274	10	US-09-923-876-5151	Sequence 5151, App
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C 275	19	1.0	3096	17	US-10-437-963-5387	Sequence 5387, App	C 348	18	0.9	278	9	US-09-974-300-6480	Sequence 6480, App
C 276	19	1.0	3517	15	US-10-104-047-102	Sequence 102, App	C 349	18	0.9	284	9	US-09-294-033B-1608	Sequence 1608, App
C 277	19	1.0	3600	15	US-10-023-888-1	Sequence 1, App1	C 350	18	0.9	297	9	US-09-294-033B-3921	Sequence 3921, App
C 278	19	1.0	3600	15	US-10-023-889-1	Sequence 1, App1	C 351	18	0.9	300	9	US-09-294-033B-1720	Sequence 1720, App
C 279	19	1.0	3600	15	US-10-023-890-1	Sequence 1, App1	C 352	18	0.9	303	9	US-09-816-279-3	Sequence 3, App1
C 280	19	1.0	3600	15	US-10-024-197-1	Sequence 1, App1	C 353	18	0.9	306	9	US-09-816-279-1	Sequence 1, App1
C 281	19	1.0	3600	15	US-10-023-894-1	Sequence 21, App1	C 354	18	0.9	319	17	US-10-437-963-21372	Sequence 21372, A
C 282	19	1.0	3621	9	US-09-895-072-21	Sequence 21, App1	C 355	18	0.9	321	9	US-09-933-797-351	Sequence 351, App
C 283	19	1.0	3621	9	US-09-895-072-21	Sequence 21, App1	C 356	18	0.9	331	18	US-10-674-124A-7446	Sequence 7446, App
C 284	19	1.0	3621	15	US-10-306-686-21	Sequence 20, App1	C 357	18	0.9	340	16	US-10-424-599-42777	Sequence 42777, A
C 285	19	1.0	3783	9	US-09-895-072-20	Sequence 20, App1	C 358	18	0.9	340	16	US-10-424-599-42777	Sequence 42777, A
C 286	19	1.0	3783	9	US-09-895-072-20	Sequence 20, App1	C 359	18	0.9	357	11	US-09-864-708-7797	Sequence 7797, App
C 287	19	1.0	3783	15	US-09-986-552-20	Sequence 20, App1	C 360	18	0.9	360	9	US-09-864-761-28274	Sequence 28274, A
C 288	19	1.0	3783	15	US-10-306-686-20	Sequence 20, App1	C 361	18	0.9	361	14	US-10-091-504-1326	Sequence 1326, App
C 289	19	1.0	4373	17	US-10-437-963-31552	Sequence 31552, A	C 362	18	0.9	361	14	US-10-091-504-1326	Sequence 1326, App
C 290	19	1.0	4413	16	US-10-424-599-14147	Sequence 14147, A	C 363	18	0.9	361	16	US-10-227-577-1326	Sequence 1326, App
C 291	19	1.0	4627	17	US-10-437-963-57509	Sequence 57509, A	C 364	18	0.9	361	16	US-10-227-577-1326	Sequence 1326, App
C 292	19	1.0	4842	17	US-10-437-963-5193	Sequence 5193, App	C 365	18	0.9	361	16	US-10-227-577-1326	Sequence 1326, App
C 293	19	1.0	5252	15	US-10-172-118-35	Sequence 35, App1	C 366	18	0.9	361	16	US-10-227-577-1326	Sequence 1326, App
C 294	19	1.0	5252	16	US-10-342-887-35	Sequence 35, App1	C 367	18	0.9	361	16	US-10-227-577-1326	Sequence 1326, App
C 295	19	1.0	5597	9	US-09-895-072-4	Sequence 4, App1	C 368	18	0.9	361	16	US-10-227-577-1326	Sequence 1326, App
C 296	19	1.0	5597	9	US-09-986-552-4	Sequence 4, App1	C 369	18	0.9	361	16	US-10-227-577-1326	Sequence 1326, App
C 297	19	1.0	5597	15	US-10-023-888-3	Sequence 3, App1	C 370	18	0.9	362	16	US-10-091-504-1325	Sequence 1325, App
C 298	19	1.0	5597	15	US-10-023-889-3	Sequence 3, App1	C 371	18	0.9	362	16	US-10-091-504-1325	Sequence 1325, App
C 299	19	1.0	5597	15	US-10-023-890-3	Sequence 3, App1	C 372	18	0.9	362	16	US-10-227-577-1325	Sequence 1325, App
C 300	19	1.0	5597	15	US-10-024-197-3	Sequence 3, App1	C 373	18	0.9	367	11	US-09-732-627A-1118	Sequence 1118, App
C 301	19	1.0	5597	15	US-10-023-894-3	Sequence 3, App1	C 374	18	0.9	375	9	US-09-864-761-17485	Sequence 17485, A
C 302	19	1.0	5597	15	US-10-306-86-4	Sequence 4, App1	C 375	18	0.9	378	11	US-09-732-627A-1464	Sequence 1464, App
C 303	19	1.0	5810	17	US-10-437-963-54024	Sequence 54024, A	C 376	18	0.9	382	10	US-09-803-719-9	Sequence 9, App1
C 304	19	1.0	6616	15	US-10-311-455-448	Sequence 448, App	C 377	18	0.9	386	11	US-09-732-627A-3915	Sequence 3915, App
C 304	19	1.0	6754	16	US-10-221-613-265	Sequence 265, App							



378	18	0.9	386	18	US-10-674-124A-23154	Sequence 23154, A
C 379	18	0.9	390	17	US-10-437-963-73339	Sequence 73339, A
C 380	18	0.9	396	17	US-10-437-963-40111	Sequence 40111, A
C 381	18	0.9	421	18	US-10-425-115-158331	Sequence 158331, A
C 382	18	0.9	430	13	US-10-027-632-83597	Sequence 83597, A
C 383	18	0.9	430	13	US-10-027-632-316141	Sequence 316141, A
C 384	18	0.9	430	15	US-10-027-632-83597	Sequence 83597, A
C 385	18	0.9	430	15	US-10-027-632-316141	Sequence 316141, A
C 386	18	0.9	430	18	US-10-674-124A-9824	Sequence 9824, A
C 387	18	0.9	438	16	US-10-424-599-27753	Sequence 27753, A
C 388	18	0.9	438	18	US-10-674-124A-21659	Sequence 21659, A
C 389	18	0.9	439	9	US-09-876-889-273	Sequence 273, App
C 390	18	0.9	441	13	US-10-027-632-41035	Sequence 41035, A
C 391	18	0.9	441	15	US-10-027-632-41035	Sequence 41035, A
C 392	18	0.9	443	16	US-10-424-599-16042	Sequence 16042, A
C 393	18	0.9	443	17	US-10-437-963-102112	Sequence 102112, A
C 394	18	0.9	450	9	US-09-864-761-11696	Sequence 11696, A
C 395	18	0.9	452	17	US-10-437-963-74371	Sequence 74371, A
C 396	18	0.9	452	18	US-10-674-124A-4960	Sequence 4960, A
C 397	18	0.9	462	16	US-10-424-599-23031	Sequence 23031, A
C 398	18	0.9	465	9	US-09-864-761-23120	Sequence 23120, A
C 399	18	0.9	470	9	US-09-864-761-2442	Sequence 2442, A
C 400	18	0.9	474	9	US-09-864-761-1685	Sequence 1685, App
C 401	18	0.9	474	9	US-09-864-761-3616	Sequence 3616, App
C 402	18	0.9	475	18	US-10-674-124A-17053	Sequence 17053, A
C 403	18	0.9	477	9	US-09-864-761-698	Sequence 698, App
C 404	18	0.9	477	9	US-09-864-761-5954	Sequence 5954, App
C 405	18	0.9	479	9	US-09-864-761-3539	Sequence 3539, App
C 406	18	0.9	481	17	US-10-767-701-25413	Sequence 25413, A
C 407	18	0.9	486	9	US-09-864-761-6405	Sequence 6405, App
C 408	18	0.9	491	16	US-10-424-599-79559	Sequence 79559, A
C 409	18	0.9	491	17	US-10-425-115-39559	Sequence 39559, A
C 410	18	0.9	493	17	US-10-021-323-9316	Sequence 9316, App
C 411	18	0.9	494	9	US-09-864-761-2947	Sequence 2947, App
C 412	18	0.9	495	18	US-10-425-115-65791	Sequence 65791, A
C 413	18	0.9	496	9	US-09-864-761-10689	Sequence 10689, A
C 414	18	0.9	499	13	US-10-027-632-136133	Sequence 136133, A
C 415	18	0.9	499	15	US-10-027-632-136133	Sequence 136133, A
C 416	18	0.9	502	17	US-10-437-963-26384	Sequence 26384, A
C 417	18	0.9	504	17	US-10-437-963-24614	Sequence 24614, A
C 418	18	0.9	511	9	US-09-864-761-18441	Sequence 18441, A
C 419	18	0.9	511	9	US-09-864-761-20384	Sequence 20384, A
C 420	18	0.9	517	16	US-10-424-599-106345	Sequence 106345, A
C 421	18	0.9	521	9	US-09-917-800A-1194	Sequence 1194, App
C 422	18	0.9	529	17	US-10-767-701-915	Sequence 915, App
C 423	18	0.9	532	17	US-10-425-114-3128	Sequence 3128, App
C 424	18	0.9	532	17	US-10-767-701-7386	Sequence 7386, A
C 425	18	0.9	533	17	US-10-437-963-9878	Sequence 9878, App
C 426	18	0.9	545	13	US-10-027-632-238238	Sequence 238238, A
C 427	18	0.9	545	15	US-10-027-632-238238	Sequence 238238, A
C 428	18	0.9	545	16	US-10-424-599-79534	Sequence 79534, A
C 429	18	0.9	560	13	US-10-027-632-260145	Sequence 260145, A
C 430	18	0.9	560	13	US-10-027-632-260146	Sequence 260146, A
C 431	18	0.9	560	15	US-10-027-632-260145	Sequence 260145, A
C 432	18	0.9	560	15	US-10-027-632-260146	Sequence 260146, A
C 433	18	0.9	560	16	US-10-425-114-27621	Sequence 27621, A
C 434	18	0.9	563	17	US-10-021-323-15398	Sequence 15398, A
C 435	18	0.9	564	15	US-10-029-386-6595	Sequence 6595, App
C 436	18	0.9	573	18	US-10-425-115-43899	Sequence 43899, A
C 437	18	0.9	582	17	US-10-767-701-1988	Sequence 1988, App
C 438	18	0.9	586	15	US-10-029-386-1030	Sequence 1030, App
C 439	18	0.9	591	17	US-10-021-323-1656	Sequence 1656, App
C 440	18	0.9	594	16	US-10-425-114-1806	Sequence 1806, App
C 441	18	0.9	596	13	US-10-027-632-270692	Sequence 270692, A
C 442	18	0.9	596	15	US-10-027-632-270692	Sequence 270692, A
C 443	18	0.9	598	15	US-10-029-386-3466	Sequence 3466, App
C 444	18	0.9	613	17	US-10-767-701-24505	Sequence 24505, A
C 445	18	0.9	614	13	US-10-027-632-3982	Sequence 3982, App
C 446	18	0.9	614	15	US-10-027-632-3982	Sequence 3982, App
C 447	18	0.9	629	15	US-10-425-115-448410	Sequence 448410, A
C 448	18	0.9	632	13	US-10-027-632-228421	Sequence 228421, A
C 449	18	0.9	632	15	US-10-029-386-228421	Sequence 228421, A
C 450	18	0.9	633	16	US-10-425-114-1974	Sequence 1974, App
451	18	0.9	636	17	US-10-767-701-25393	Sequence 25393, A
C 452	18	0.9	637	17	US-10-767-701-13942	Sequence 13942, A
C 453	18	0.9	640	16	US-10-424-599-3769	Sequence 3769, A
C 454	18	0.9	642	17	US-10-021-323-8680	Sequence 8680, App
C 455	18	0.9	643	17	US-10-767-701-9329	Sequence 9329, App
C 456	18	0.9	644	17	US-10-767-701-26613	Sequence 26613, A
C 457	18	0.9	647	17	US-10-767-701-26061	Sequence 26061, A
C 458	18	0.9	657	9	US-09-833-381-921	Sequence 921, App
C 459	18	0.9	658	16	US-10-425-114-20639	Sequence 20639, A
C 460	18	0.9	659	17	US-10-767-701-12351	Sequence 12351, A
C 461	18	0.9	662	13	US-10-027-632-172453	Sequence 172453, A
C 462	18	0.9	662	15	US-10-027-632-172453	Sequence 172453, A
C 463	18	0.9	664	10	US-09-919-039-261	Sequence 261, App
C 464	18	0.9	676	13	US-10-027-632-234699	Sequence 234699, A
C 465	18	0.9	676	15	US-10-027-632-234699	Sequence 234700, A
C 466	18	0.9	676	15	US-10-027-632-234699	Sequence 234699, A
C 467	18	0.9	676	15	US-10-027-632-234700	Sequence 234700, A
C 468	18	0.9	678	16	US-10-425-114-30644	Sequence 30644, A
C 469	18	0.9	683	18	US-10-425-115-43821	Sequence 43821, A
C 470	18	0.9	683	18	US-10-425-115-52891	Sequence 52891, A
C 471	18	0.9	691	14	US-10-198-846-11852	Sequence 11852, A
C 472	18	0.9	697	18	US-10-425-115-94860	Sequence 94860, A
C 473	18	0.9	704	17	US-10-767-701-5945	Sequence 5945, App
C 474	18	0.9	708	13	US-10-027-632-28298	Sequence 28298, A
C 475	18	0.9	708	15	US-10-027-632-28298	Sequence 28298, A
C 476	18	0.9	719	18	US-10-425-115-163175	Sequence 163175, A
C 477	18	0.9	721	18	US-10-425-115-126748	Sequence 126748, A
C 478	18	0.9	729	16	US-10-424-599-109452	Sequence 109452, A
C 479	18	0.9	734	16	US-10-424-599-4027	Sequence 4027, App
C 480	18	0.9	742	18	US-10-425-115-125730	Sequence 125730, A
C 481	18	0.9	746	9	US-09-910-943-885	Sequence 485, App
C 482	18	0.9	746	17	US-10-767-701-13193	Sequence 13193, A
C 483	18	0.9	747	17	US-10-437-963-50399	Sequence 50399, A
C 484	18	0.9	760	18	US-10-425-115-29176	Sequence 29176, A
C 485	18	0.9	769	18	US-10-739-930-4340	Sequence 4340, App
C 486	18	0.9	775	17	US-10-437-963-90950	Sequence 90950, A
C 487	18	0.9	777	18	US-10-425-115-80497	Sequence 80497, A
C 488	18	0.9	778	16	US-10-424-599-13897	Sequence 13897, A
C 489	18	0.9	794	13	US-10-027-632-8651	Sequence 8651, App
C 490	18	0.9	794	15	US-10-027-632-8652	Sequence 8652, App
C 491	18	0.9	794	15	US-10-027-632-8651	Sequence 8651, App
C 492	18	0.9	794	15	US-10-027-632-8652	Sequence 8652, App
C 493	18	0.9	801	15	US-10-259-165-429	Sequence 429, App
C 494	18	0.9	809	16	US-10-425-114-8763	Sequence 8763, App
C 495	18	0.9	814	17	US-10-437-963-73949	Sequence 73949, A
C 496	18	0.9	825	17	US-10-437-963-99757	Sequence 99757, A
C 497	18	0.9	828	17	US-10-437-963-99757	Sequence 99757, A
C 498	18	0.9	832	17	US-10-767-701-11455	Sequence 11455, A
C 499	18	0.9	839	9	US-09-974-300-6508	Sequence 6508, App
C 500	18	0.9	839	9	US-09-974-300-6508	Sequence 6508, App
C 501	18	0.9	839	9	US-10-425-115-132071	Sequence 132071, A
C 502	18	0.9	849	14	US-10-198-846-3519	Sequence 3519, App
C 503	18	0.9	849	14	US-10-198-846-3519	Sequence 3519, App
C 504	18	0.9	851	16	US-10-425-115-53800	Sequence 53800, A
C 505	18	0.9	851	16	US-10-424-599-14725	Sequence 14725, A
C 506	18	0.9	855	18	US-10-425-115-132419	Sequence 132419, A
C 507	18	0.9	861	9	US-09-938-842A-2206	Sequence 2206, App
C 508	18	0.9	861	11	US-09-938-842A-2206	Sequence 2206, App
C 509	18	0.9	863	13	US-10-027-632-156867	Sequence 156867, A
C 510	18	0.9	863	13	US-10-027-632-156867	Sequence 156867, A
C 511	18	0.9	863	13	US-10-027-632-156867	Sequence 156867, A
C 512	18	0.9	863	15	US-10-027-632-156867	Sequence 156867, A
C 513	18	0.9	863	15	US-10-027-632-156867	Sequence 156867, A
C 514	18	0.9	863	15	US-10-027-632-156869	Sequence 156869, A
C 515	18	0.9	864	17	US-10-437-963-11202	Sequence 11202, A
C 516	18	0.9	873	13	US-10-027-632-121821	Sequence 121821, A
C 517	18	0.9	873	13	US-10-027-632-121821	Sequence 121821, A
C 518	18	0.9	877	17	US-10-767-701-738	Sequence 738, App
C 519	18	0.9	880	16	US-09-815-153-4	Sequence 4, App1
C 520	18	0.9	890	16	US-10-428-487-21	Sequence 21, App1
C 521	18	0.9	890	17	US-10-437-963-48197	Sequence 48197, A
C 522	18	0.9	903	15	US-10-029-386-10462	Sequence 10462, A
C 523	18	0.9	904	16	US-10-425-114-19583	Sequence 19583, A

C 524	18	0.9	904	18	US-10-425-115-23909	Sequence 23909, A
C 525	18	0.9	910	9	US-09-880-107-1602	Sequence 1602, Ap
526	18	0.9	910	13	US-10-027-632-162147	Sequence 162147, A
527	18	0.9	910	15	US-10-027-632-162147	Sequence 162147, A
528	18	0.9	936	18	US-10-425-115-5837	Sequence 5837, Ap
C 529	18	0.9	956	17	US-10-437-963-19506	Sequence 19506, A
C 530	18	0.9	957	18	US-10-739-930-2223	Sequence 2223, Ap
C 531	18	0.9	960	17	US-10-437-963-60424	Sequence 60424, Ap
C 532	18	0.9	963	17	US-10-437-963-82835	Sequence 82835, A
C 533	18	0.9	972	16	US-10-424-599-14296	Sequence 14296, A
534	18	0.9	1008	16	US-10-464-610-1	Sequence 1, Appl1
535	18	0.9	1014	16	US-10-320-797-2131	Sequence 2131, Ap
C 536	18	0.9	1030	18	US-10-425-115-25644	Sequence 25644, A
C 537	18	0.9	1036	16	US-10-424-599-32223	Sequence 32223, A
C 538	18	0.9	1048	15	US-10-369-493-27877	Sequence 27877, A
C 539	18	0.9	1058	18	US-10-425-115-73539	Sequence 73539, A
540	18	0.9	1060	18	US-10-425-115-128138	Sequence 128138, A
541	18	0.9	1110	15	US-10-411-224-11	Sequence 11, Appl1
542	18	0.9	1110	16	US-10-047-021-11	Sequence 11, Appl1
C 543	18	0.9	1116	16	US-10-425-115-9652	Sequence 9652, Ap
544	18	0.9	1117	18	US-10-425-115-128136	Sequence 128136, A
C 545	18	0.9	1123	18	US-10-425-115-69967	Sequence 69967, A
C 546	18	0.9	1132	16	US-10-424-599-119632	Sequence 119632, A
547	18	0.9	1134	16	US-10-424-599-119632	Sequence 119632, A
C 548	18	0.9	1143	15	US-10-369-493-27834	Sequence 27834, A
549	18	0.9	1149	10	US-09-910-186A-27	Sequence 27, Appl1
C 550	18	0.9	1149	13	US-10-027-632-10356	Sequence 10356, A
C 551	18	0.9	1149	13	US-10-027-632-10357	Sequence 10357, A
C 552	18	0.9	1149	13	US-10-027-632-10358	Sequence 10358, A
C 553	18	0.9	1149	15	US-10-027-632-10356	Sequence 10356, A
C 554	18	0.9	1149	15	US-10-027-632-10357	Sequence 10357, A
C 555	18	0.9	1149	15	US-10-027-632-10358	Sequence 10358, A
C 556	18	0.9	1174	17	US-10-767-701-8200	Sequence 8200, Ap
C 557	18	0.9	1181	16	US-10-415-134-3	Sequence 3, Appl1
C 558	18	0.9	1218	16	US-10-425-114-27112	Sequence 27112, A
C 559	18	0.9	1219	18	US-10-425-115-58743	Sequence 58743, A
C 560	18	0.9	1224	17	US-10-437-963-11898	Sequence 11898, A
C 561	18	0.9	1232	18	US-10-425-115-157174	Sequence 157174, A
562	18	0.9	1246	17	US-10-437-963-56227	Sequence 56227, A
563	18	0.9	1267	17	US-10-767-701-10493	Sequence 10493, A
C 564	18	0.9	1272	17	US-10-767-701-10463	Sequence 10463, A
565	18	0.9	1273	16	US-10-425-114-35619	Sequence 35619, A
C 566	18	0.9	1273	17	US-10-437-963-44884	Sequence 44884, A
C 567	18	0.9	1275	17	US-10-437-963-49222	Sequence 49233, A
C 568	18	0.9	1286	17	US-10-437-963-45794	Sequence 45794, A
C 569	18	0.9	1295	16	US-10-282-122A-20115	Sequence 20115, A
C 570	18	0.9	1323	17	US-10-437-963-49235	Sequence 49235, A
571	18	0.9	1355	16	US-10-425-114-25775	Sequence 25775, A
C 572	18	0.9	1364	17	US-10-437-963-76875	Sequence 76875, A
573	18	0.9	1376	18	US-10-425-115-112979	Sequence 112979, A
C 574	18	0.9	1380	16	US-10-424-599-54926	Sequence 54926, A
C 575	18	0.9	1380	17	US-10-437-963-12714	Sequence 12714, A
C 576	18	0.9	1387	17	US-10-437-963-88707	Sequence 88707, A
C 577	18	0.9	1390	10	US-09-933-767-124	Sequence 124, App
C 578	18	0.9	1390	14	US-10-004-860-124	Sequence 124, App
C 579	18	0.9	1392	14	US-10-023-282-124	Sequence 124, App
580	18	0.9	1399	16	US-10-320-797-1131	Sequence 1131, Ap
C 581	18	0.9	1401	16	US-10-424-599-89804	Sequence 89804, A
C 582	18	0.9	1408	16	US-10-425-114-15596	Sequence 15596, A
C 583	18	0.9	1417	18	US-10-425-115-52892	Sequence 52892, A
C 584	18	0.9	1452	18	US-10-793-639-317	Sequence 317, App
585	18	0.9	1464	17	US-10-437-963-7077	Sequence 7077, Ap
C 586	18	0.9	1471	16	US-10-424-599-129382	Sequence 129382, A
C 587	18	0.9	1520	18	US-10-739-930-1666	Sequence 1666, Ap
588	18	0.9	1525	16	US-10-424-599-23293	Sequence 23293, A
C 589	18	0.9	1539	18	US-10-425-115-36325	Sequence 36325, A
590	18	0.9	1544	16	US-10-276-774-982	Sequence 982, App
C 591	18	0.9	1554	17	US-10-032-585-6874	Sequence 6874, Ap
592	18	0.9	1563	15	US-10-437-963-102018	Sequence 102018, A
593	18	0.9	1580	18	US-10-425-115-128137	Sequence 128137, A
594	18	0.9	1590	18	US-10-424-599-39222	Sequence 39222, A
595	18	0.9	1597	17	US-10-437-963-53894	Sequence 53894, A
596	18	0.9	1621	16	US-10-425-114-3084	Sequence 3084, Ap
597	18	0.9	1638	16	US-10-425-114-11638	Sequence 11638, A
598	18	0.9	1645	16	US-10-424-599-110728	Sequence 110728, A
599	18	0.9	1656	16	US-10-425-114-34761	Sequence 34761, A
600	18	0.9	1662	16	US-10-425-114-33883	Sequence 33883, A
601	18	0.9	1669	17	US-10-437-963-69399	Sequence 69399, A
C 602	18	0.9	1680	13	US-10-027-632-264413	Sequence 264413, A
C 603	18	0.9	1680	15	US-10-027-632-264413	Sequence 264413, A
604	18	0.9	1684	9	US-09-764-877-3818	Sequence 3818, Ap
605	18	0.9	1684	16	US-10-242-515-2818	Sequence 2818, Ap
606	18	0.9	1719	16	US-10-425-114-28183	Sequence 28183, A
C 607	18	0.9	1734	15	US-10-172-118-1726	Sequence 1726, Ap
C 608	18	0.9	1734	16	US-10-342-887-1726	Sequence 1726, Ap
C 609	18	0.9	1751	17	US-10-437-963-9763	Sequence 9763, Ap
610	18	0.9	1753	16	US-10-437-963-35008	Sequence 35008, A
611	18	0.9	1759	16	US-10-425-114-14300	Sequence 340, App
612	18	0.9	1769	18	US-10-425-115-65582	Sequence 65582, A
613	18	0.9	1774	18	US-10-425-115-147000	Sequence 147000, A
C 614	18	0.9	1777	18	US-10-425-115-122008	Sequence 122008, A
615	18	0.9	1787	18	US-10-425-115-81653	Sequence 81653, A
616	18	0.9	1799	17	US-10-437-963-20536	Sequence 20536, A
617	18	0.9	1806	18	US-10-425-115-176673	Sequence 176673, A
C 618	18	0.9	1840	11	US-02-973-278-921	Sequence 921, App
619	18	0.9	1846	17	US-10-437-963-92205	Sequence 92205, A
620	18	0.9	1849	17	US-10-437-963-21003	Sequence 21003, A
C 621	18	0.9	1862	18	US-10-425-115-147001	Sequence 147001, A
C 622	18	0.9	1878	11	US-09-938-842A-1413	Sequence 1413, Ap
C 623	18	0.9	1878	9	US-09-938-842A-1413	Sequence 1413, Ap
624	18	0.9	1895	16	US-10-424-599-117416	Sequence 117416, A
C 625	18	0.9	1910	13	US-10-027-632-99815	Sequence 99815, A
C 626	18	0.9	1910	13	US-10-027-632-99816	Sequence 99816, A
C 627	18	0.9	1910	13	US-10-027-632-99817	Sequence 99817, A
C 628	18	0.9	1910	15	US-10-027-632-99815	Sequence 99815, A
C 629	18	0.9	1910	15	US-10-027-632-99816	Sequence 99816, A
C 630	18	0.9	1910	15	US-10-027-632-99817	Sequence 99817, A
631	18	0.9	1925	15	US-10-369-493-55962	Sequence 55962, A
632	18	0.9	1933	17	US-10-437-963-6806	Sequence 6806, Ap
633	18	0.9	1935	16	US-10-424-599-138002	Sequence 138002, A
C 634	18	0.9	1941	17	US-10-437-963-5385	Sequence 5385, Ap
C 635	18	0.9	1962	9	US-09-938-842A-2542	Sequence 2542, Ap
C 636	18	0.9	1962	11	US-10-108-260A-129	Sequence 129, App
C 637	18	0.9	1969	16	US-09-938-842A-2542	Sequence 2542, Ap
C 638	18	0.9	1986	9	US-09-767-870-4	Sequence 4, Appl1
C 639	18	0.9	1986	15	US-10-242-568-4	Sequence 4, Appl1
C 640	18	0.9	1986	16	US-10-425-114-15609	Sequence 15609, A
641	18	0.9	1986	15	US-10-425-114-174166	Sequence 174166, A
642	18	0.9	2000	11	US-09-938-842A-4104	Sequence 4104, Ap
643	18	0.9	2007	16	US-10-425-114-3832	Sequence 3832, Ap
C 644	18	0.9	2038	9	US-09-880-107-1102	Sequence 1102, Ap
C 645	18	0.9	2056	17	US-10-437-963-72774	Sequence 72774, A
646	18	0.9	2061	17	US-10-437-963-71684	Sequence 71684, A
C 647	18	0.9	2061	17	US-10-437-963-71684	Sequence 71684, A
648	18	0.9	2065	16	US-10-425-114-35471	Sequence 35471, A
649	18	0.9	2067	15	US-10-310-154-54	Sequence 54, Appl1
C 650	18	0.9	2093	15	US-10-037-270-999	Sequence 999, App
C 651	18	0.9	2093	15	US-10-117-722-999	Sequence 999, App
C 652	18	0.9	2102	15	US-10-104-047-1274	Sequence 1274, Ap
C 653	18	0.9	2112	17	US-10-437-963-101275	Sequence 101275, A
654	18	0.9	2122	18	US-10-425-115-119650	Sequence 119650, A
655	18	0.9	2132	17	US-10-767-701-13570	Sequence 13570, A
656	18	0.9	2145	17	US-10-437-963-12104	Sequence 12104, A
657	18	0.9	2152	16	US-10-424-599-90186	Sequence 90186, A
658	18	0.9	2157	17	US-10-437-963-38370	Sequence 38370, A
C 659	18	0.9	2187	17	US-10-437-963-5708	Sequence 5708, Ap
C 660	18	0.9	2216	17	US-10-437-963-53764	Sequence 53764, A
C 661	18	0.9	2220	17	US-10-437-963-37476	Sequence 37476, A
C 662	18	0.9	2221	17	US-10-437-963-23020	Sequence 23020, A
C 663	18	0.9	2241	17	US-10-437-963-2339	Sequence 2339, Ap
C 664	18	0.9	2247	17	US-10-437-963-8518	Sequence 8518, Ap
C 665	18	0.9	2282	18	US-10-425-115-47395	Sequence 47395, A
C 666	18	0.9	2282	18	US-10-425-115-163176	Sequence 163176, A
C 667	18	0.9	2321	18	US-10-425-115-29174	Sequence 29174, A
C 668	18	0.9	2368	18	US-10-425-115-43614	Sequence 43614, A
C 669	18	0.9	2372	18	US-10-425-115-43614	Sequence 43614, A

C 670	18	0.9	2378	17	US-10-437-963-32722	Sequence 32722, A
C 671	18	0.9	2385	15	US-10-156-761-6087	Sequence 6087, Ap
C 672	18	0.9	2397	17	US-10-437-963-97634	Sequence 97634, A
C 673	18	0.9	2415	13	US-10-011-588-36	Sequence 36, Appl
C 674	18	0.9	2431	9	US-09-880-107-2266	Sequence 2266, Ap
C 675	18	0.9	2431	16	US-10-641-643-1198	Sequence 1198, Ap
C 676	18	0.9	2433	18	US-10-425-115-26477	Sequence 26477, A
C 677	18	0.9	2442	16	US-10-424-599-139178	Sequence 139178, A
C 678	18	0.9	2451	16	US-10-424-599-95479	Sequence 95479, A
C 679	18	0.9	2454	15	US-10-168-09A-75	Sequence 75, Appl
C 680	18	0.9	2475	17	US-10-437-963-38377	Sequence 38377, A
C 681	18	0.9	2476	17	US-10-437-963-85552	Sequence 85552, A
C 682	18	0.9	2526	17	US-10-437-963-38425	Sequence 38425, A
C 683	18	0.9	2527	17	US-10-437-963-1559	Sequence 1559, Ap
C 684	18	0.9	2543	16	US-10-062-674-1655	Sequence 1655, Ap
C 685	18	0.9	2548	18	US-10-425-115-29173	Sequence 29173, A
C 686	18	0.9	2559	16	US-10-412-699B-771	Sequence 771, Ap
C 687	18	0.9	2591	13	US-10-027-632-112013	Sequence 112013, A
C 688	18	0.9	2591	13	US-10-027-632-112014	Sequence 112014, A
C 689	18	0.9	2591	15	US-10-027-632-112013	Sequence 112013, A
C 690	18	0.9	2591	15	US-10-027-632-112014	Sequence 112014, A
C 691	18	0.9	2610	15	US-10-278-536-236	Sequence 236, Ap
C 692	18	0.9	2617	15	US-10-176-277-4	Sequence 4, Appl
C 693	18	0.9	2621	17	US-10-437-963-54834	Sequence 54834, A
C 694	18	0.9	2628	17	US-10-437-963-62156	Sequence 62156, A
C 695	18	0.9	2633	11	US-09-973-278-920	Sequence 920, Ap
C 696	18	0.9	2646	17	US-10-437-963-10376	Sequence 10376, A
C 697	18	0.9	2655	16	US-10-424-599-57846	Sequence 57846, A
C 698	18	0.9	2655	16	US-10-425-114-7339	Sequence 7339, Ap
C 699	18	0.9	2682	14	US-10-170-656-8	Sequence 8, Appl
C 700	18	0.9	2688	17	US-10-437-963-38454	Sequence 38454, A
C 701	18	0.9	2706	17	US-10-437-963-7022	Sequence 7022, Ap
C 702	18	0.9	2735	17	US-10-437-963-94592	Sequence 94592, A
C 703	18	0.9	2820	17	US-10-437-963-76755	Sequence 76755, A
C 704	18	0.9	2826	9	US-09-925-297-403	Sequence 293, App
C 705	18	0.9	2826	15	US-10-320-585-6930	Sequence 6930, App
C 706	18	0.9	2829	16	US-10-320-797-131	Sequence 131, App
C 707	18	0.9	3018	13	US-10-027-632-114681	Sequence 114681, A
C 708	18	0.9	3018	15	US-10-027-632-114681	Sequence 114681, A
C 709	18	0.9	3051	18	US-10-425-115-43605	Sequence 43605, A
C 710	18	0.9	3055	18	US-10-425-115-128140	Sequence 128140, A
C 711	18	0.9	3092	13	US-10-027-632-264858	Sequence 264858, A
C 712	18	0.9	3092	13	US-10-027-632-264859	Sequence 264859, A
C 713	18	0.9	3092	15	US-10-027-632-264858	Sequence 264858, A
C 714	18	0.9	3092	15	US-10-027-632-264858	Sequence 264858, A
C 715	18	0.9	3092	15	US-10-027-632-264858	Sequence 264858, A
C 716	18	0.9	3092	15	US-10-027-632-264858	Sequence 264858, A
C 717	18	0.9	3158	17	US-10-437-963-34020	Sequence 34020, A
C 718	18	0.9	3158	17	US-10-437-963-34020	Sequence 34020, A
C 719	18	0.9	3290	17	US-10-437-963-3759	Sequence 3759, Ap
C 720	18	0.9	3493	17	US-10-437-963-83811	Sequence 83811, A
C 721	18	0.9	3594	17	US-10-437-963-51978	Sequence 51978, A
C 722	18	0.9	3594	17	US-10-437-963-51978	Sequence 51978, A
C 723	18	0.9	3787	10	US-09-930-213-284	Sequence 284, App
C 724	18	0.9	4080	9	US-09-833-381-922	Sequence 922, App
C 725	18	0.9	4479	16	US-10-346-198-79	Sequence 79, Appl
C 726	18	0.9	4817	10	US-09-988-462-18	Sequence 462, App
C 727	18	0.9	4840	17	US-10-437-963-72826	Sequence 72826, A
C 728	18	0.9	5677	18	US-10-788-792-45	Sequence 45, Appl
C 729	18	0.9	7263	15	US-10-037-270-55	Sequence 55, Appl
C 730	18	0.9	7263	15	US-10-037-270-55	Sequence 55, Appl
C 731	18	0.9	7791	16	US-10-117-722-55	Sequence 35, Appl
C 732	18	0.9	7791	16	US-10-375-253-35	Sequence 33, Appl
C 733	18	0.9	7808	15	US-10-375-253-35	Sequence 33, Appl
C 734	18	0.9	7827	15	US-10-101-510-422	Sequence 422, App
C 735	18	0.9	12374	15	US-10-017-161-1097	Sequence 1097, Ap
C 736	18	0.9	14770	11	US-10-292-798-933	Sequence 933, App
C 737	18	0.9	14770	11	US-09-873-367C-230	Sequence 230, App
C 738	18	0.9	14770	11	US-09-968-007A-124	Sequence 124, App
C 739	18	0.9	14770	11	US-09-968-007A-405	Sequence 405, App
C 740	18	0.9	14770	15	US-10-172-118-1848	Sequence 1848, Ap
C 741	18	0.9	15439	9	US-10-342-887-1848	Sequence 1848, Ap
C 742	18	0.9	15439	14	US-09-764-884-36	Sequence 36, Appl
C 743	18	0.9	15439	14	US-10-092-256-36	Sequence 36, Appl
C 743	18	0.9	16556	15	US-10-132-720-3	Sequence 3, Appl
C 744	18	0.9	17491	15	US-10-017-161-1995	Sequence 1995, Ap
C 745	18	0.9	19803	15	US-10-017-161-1023	Sequence 1023, Ap
C 746	18	0.9	23871	13	US-10-087-192-703	Sequence 703, App
C 747	18	0.9	26429	17	US-10-322-696-106	Sequence 106, App
C 748	18	0.9	26991	13	US-10-087-192-24	Sequence 24, Appl
C 749	18	0.9	44128	17	US-10-367-094-23	Sequence 23, Appl
C 750	18	0.9	44853	17	US-10-367-281-627	Sequence 627, App
C 751	18	0.9	61791	17	US-10-322-281-645	Sequence 645, App
C 752	18	0.9	61955	17	US-10-292-798-449	Sequence 449, App
C 753	18	0.9	67191	15	US-09-997-722-169	Sequence 169, App
C 754	18	0.9	87394	18	US-10-105-612-1	Sequence 1, Appl
C 755	18	0.9	90501	17	US-10-810-788A-6	Sequence 6, Appl
C 756	18	0.9	90501	17	US-10-367-094-166	Sequence 166, App
C 757	18	0.9	96592	11	US-10-174-020-11	Sequence 11, Appl
C 758	18	0.9	96592	11	US-09-997-722-88	Sequence 88, Appl
C 759	18	0.9	108316	15	US-10-017-724-3	Sequence 3, Appl
C 760	18	0.9	108316	15	US-10-292-798-1789	Sequence 1789, Ap
C 761	18	0.9	108316	15	US-10-017-161-2143	Sequence 2143, Ap
C 762	18	0.9	113585	16	US-10-188-470-12	Sequence 12, Appl
C 763	18	0.9	127917	17	US-10-775-169-82	Sequence 82, Appl
C 764	18	0.9	143306	9	US-09-729-920-3	Sequence 3, Appl
C 765	18	0.9	145025	13	US-10-087-192-1051	Sequence 1051, Ap
C 766	18	0.9	145068	17	US-10-322-281-33	Sequence 33, Appl
C 767	18	0.9	174566	14	US-10-020-141-1	Sequence 1, Appl
C 768	18	0.9	174566	16	US-10-235-192A-37	Sequence 37, Appl
C 769	18	0.9	219352	17	US-10-322-281-45	Sequence 45, Appl
C 770	18	0.9	339234	17	US-10-322-696-73	Sequence 73, Appl
C 771	18	0.9	374849	13	US-10-087-192-1627	Sequence 1627, Ap
C 772	18	0.9	1830121	14	US-10-329-960-1	Sequence 1, Appl
C 773	18	0.9	1830121	16	US-10-329-960-1	Sequence 1, Appl
C 774	18	0.9	1830121	16	US-10-158-865-1	Sequence 1, Appl
C 775	18	0.9	2256646	17	US-10-470-565-1	Sequence 1, Appl
C 776	18	0.9	3673778	15	US-10-312-841-1	Sequence 1, Appl
C 777	18	0.9	9025608	15	US-10-156-761-1	Sequence 1, Appl
C 778	17	0.9	25	9	US-10-098-263B-52076	Sequence 52076, A
C 779	17	0.9	39	9	US-09-263-959-203	Sequence 203, App
C 780	17	0.9	46	10	US-09-263-959-111	Sequence 111, App
C 781	17	0.9	60	10	US-09-908-975-18824	Sequence 18824, A
C 782	17	0.9	65	15	US-10-032-585-3004	Sequence 3004, A
C 783	17	0.9	98	15	US-10-029-386-22401	Sequence 22401, A
C 784	17	0.9	99	15	US-10-029-386-17340	Sequence 17340, A
C 785	17	0.9	111	9	US-09-783-590-1305	Sequence 783, App
C 786	17	0.9	114	9	US-09-969-373-786	Sequence 786, App
C 787	17	0.9	117	9	US-09-864-761-2746	Sequence 2746, A
C 788	17	0.9	118	9	US-09-864-761-29612	Sequence 29612, A
C 789	17	0.9	121	9	US-09-728-446-372	Sequence 372, App
C 790	17	0.9	121	16	US-10-424-599-71916	Sequence 71916, A
C 791	17	0.9	126	16	US-10-305-720-527	Sequence 527, App
C 792	17	0.9	128	15	US-09-864-761-23270	Sequence 23270, A
C 793	17	0.9	128	15	US-10-029-386-21970	Sequence 21970, A
C 794	17	0.9	132	9	US-09-864-761-16931	Sequence 16931, A
C 795	17	0.9	136	16	US-10-424-599-29426	Sequence 29426, A
C 796	17	0.9	142	16	US-10-242-535A-5592	Sequence 5592, Ap
C 797	17	0.9	142	16	US-10-085-783A-5592	Sequence 5592, Ap
C 798	17	0.9	152	10	US-09-754-853A-81	Sequence 81, Appl
C 799	17	0.9	156	9	US-09-864-761-22124	Sequence 22124, A
C 800	17	0.9	157	9	US-09-864-761-24600	Sequence 24600, A
C 801	17	0.9	166	15	US-09-864-761-24600	Sequence 24600, A
C 802	17	0.9	166	15	US-09-864-761-24600	Sequence 24600, A
C 803	17	0.9	167	18	US-10-029-386-26515	Sequence 26515, A
C 804	17	0.9	167	18	US-09-969-896-6	Sequence 6, Appl
C 805	17	0.9	170	17	US-10-631-958-6	Sequence 6, Appl
C 806	17	0.9	173	16	US-10-437-963-7372	Sequence 7372, Ap
C 807	17	0.9	173	16	US-10-437-963-7372	Sequence 7372, Ap
C 808	17	0.9	174	16	US-10-424-599-115729	Sequence 115729, A
C 809	17	0.9	175	16	US-10-242-535A-369	Sequence 369, A
C 810	17	0.9	175	16	US-10-242-535A-369	Sequence 369, App
C 811	17	0.9	179	9	US-10-085-783A-369	Sequence 369, App
C 812	17	0.9	184	9	US-09-728-446-1390	Sequence 1390, App
C 813	17	0.9	184	16	US-09-864-761-26724	Sequence 26724, A
C 814	17	0.9	187	16	US-10-467-019-11	Sequence 11, Appl
C 815	17	0.9	189	9	US-09-864-761-22687	Sequence 22687, A

C 816	17	0.9	198	9	US-09-864-761-28856	Sequence 28856, A	C 889	17	0.9	349	9	US-09-864-761-4816	Sequence 4816, Ap
C 817	17	0.9	216	16	US-10-424-599-63853	Sequence 63853, Ap	C 890	17	0.9	354	18	US-10-425-115-99860	Sequence 99860, A
C 818	17	0.9	219	17	US-10-437-963-62606	Sequence 62606, A	C 891	17	0.9	357	15	US-10-116-712-14	Sequence 34, App1
C 819	17	0.9	223	15	US-10-029-386-17312	Sequence 17312, A	C 892	17	0.9	358	16	US-10-424-599-33286	Sequence 33286, A
C 820	17	0.9	224	18	US-10-425-115-39119	Sequence 39119, A	C 893	17	0.9	360	17	US-10-437-963-70228	Sequence 70228, A
C 821	17	0.9	225	9	US-09-864-761-29376	Sequence 29276, A	C 894	17	0.9	361	9	US-09-796-692-7449	Sequence 7449, Ap
C 822	17	0.9	227	18	US-10-674-124A-6230	Sequence 6230, Ap	C 895	17	0.9	361	14	US-10-040-862-7449	Sequence 7449, Ap
C 823	17	0.9	229	17	US-10-437-963-83335	Sequence 83335, A	C 896	17	0.9	361	16	US-10-057-475B-7449	Sequence 7449, Ap
C 824	17	0.9	231	18	US-10-674-124A-865	Sequence 19928, A	C 897	17	0.9	361	17	US-10-154-864B-7449	Sequence 7449, Ap
C 825	17	0.9	232	9	US-09-864-761-19928	Sequence 17, App1	C 898	17	0.9	363	14	US-10-764-324-7449	Sequence 7449, Ap
C 826	17	0.9	233	9	US-09-923-876-17	Sequence 17, App1	C 899	17	0.9	363	14	US-10-231-411-3	Sequence 3, App1
C 827	17	0.9	233	10	US-09-923-876-17	Sequence 17, App1	C 900	17	0.9	363	17	US-10-437-963-73118	Sequence 73138, A
C 828	17	0.9	234	9	US-09-864-761-19661	Sequence 19061, A	C 901	17	0.9	366	17	US-09-864-761-2812	Sequence 2812, Ap
C 829	17	0.9	241	16	US-10-424-599-90106	Sequence 90106, A	C 902	17	0.9	367	18	US-10-425-115-114426	Sequence 114426, Ap
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C 839	17	0.9	261	9	US-09-864-761-17114	Sequence 977, App	C 912	17	0.9	381	9	US-09-864-761-2610	Sequence 26681, A
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C 982	17	0.9	431	15	US-10-029-386-14336
C 983	17	0.9	431	16	US-10-425-114-12426
C 984	17	0.9	432	17	US-10-437-963-70947
C 985	17	0.9	432	17	US-10-425-115-46785
C 986	17	0.9	433	10	US-09-918-995-5616
C 987	17	0.9	433	18	US-10-674-124A-2413
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C 990	17	0.9	438	17	US-10-437-963-48033
C 991	17	0.9	442	18	US-10-674-124A-2514
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C 993	17	0.9	445	9	US-09-864-761-5262
C 994	17	0.9	447	10	US-09-918-995-13670
C 995	17	0.9	447	17	US-10-437-963-18733
C 996	17	0.9	450	16	US-10-449-857A-76
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# ALIGNMENTS

RESULT 1  
 US-10-086-464-1  
 Sequence 1, Application US/10086464  
 Publication No. US20020199218A1  
 GENERAL INFORMATION:  
 APPLICANT: GORING, Daphne R. et al.  
 TITLE OF INVENTION: PROLINE-RICH EXTENSIN-LIKE RECEPTOR KINASES  
 FILE REFERENCE: P 25,762-A USA  
 CURRENT APPLICATION NUMBER: US/10/086,464  
 CURRENT FILING DATE: 2002-02-28  
 PRIOR APPLICATION NUMBER: US 10/069,304  
 PRIOR FILING DATE: 2002-02-19  
 PRIOR APPLICATION NUMBER: PCT/CA00/00966  
 PRIOR FILING DATE: 2000-08-18  
 PRIOR APPLICATION NUMBER: US 60/149,466  
 PRIOR FILING DATE: 1999-08-19  
 PRIOR APPLICATION NUMBER: US 60/159,122  
 PRIOR FILING DATE: 1999-10-13  
 NUMBER OF SEQ ID NOS: 27  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO 1  
 LENGTH: 1944  
 TYPE: DNA  
 ORGANISM: Brassica napus  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: (1)..(1944)  
 US-10-086-464-1

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 Sequence 867, App  
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 Sequence 2143, App  
 Sequence 140627, A  
 Sequence 25190, A  
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 Sequence 25514, A  
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 Sequence 76, App  
 Sequence 92, App  
 Sequence 27890, A  
 Sequence 100953, A

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Best Local Similarity 100.0%; Pred. No. 0.0044;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 203 TTTGAAGCTAAGTTGCTGATTTGG 228

## RESULT 5

US-09-923-876-5096  
; Sequence 5096, Application US/09923876  
; Publication No. US20030237110A9  
; GENERAL INFORMATION:  
; APPLICANT: Laligudi, Raghnath V.  
; APPLICANT: Kamigaki, Laura Y. (lto)  
; APPLICANT: Sherman, Bradley K.  
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING  
; FILE REFERENCE: PL-0012-1 CON  
; CURRENT APPLICATION NUMBER: US/09/923,876  
; CURRENT FILING DATE: 2001-08-06  
; PRIOR APPLICATION NUMBER: 09/298,329  
; PRIOR FILING DATE: 1999-04-21  
; PRIOR APPLICATION NUMBER: 60/085,331  
; PRIOR FILING DATE: 1998-05-05  
; NUMBER OF SEQ ID NOS: 6332  
; SOFTWARE: PERL Program  
; SEQ ID NO 5096  
; LENGTH: 268  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No. US20030237110A9 700456354H1  
; NAME/KEY: unsure  
; LOCATION: 63  
; OTHER INFORMATION: a, t, c, g, or other  
US-09-923-876-5096

Query Match  
Best Local Similarity 1.3%; Score 26; DB 10; Length 268;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 203 TTTGAAGCTAAGTTGCTGATTTGG 228

## RESULT 6

US-10-767-701-5803  
; Sequence 5803, Application US/10767701  
; Publication No. US20040172684A1  
; GENERAL INFORMATION:  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
; FILE REFERENCE: 38-21(53535)B  
; CURRENT APPLICATION NUMBER: US/10/767,701  
; CURRENT FILING DATE: 2004-01-29  
; NUMBER OF SEQ ID NOS: 63128  
; SEQ ID NO 5803  
; LENGTH: 808  
; TYPE: DNA  
; ORGANISM: Sorghum bicolor  
; FEATURE:  
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS25481\_1  
US-10-767-701-5803

Query Match  
Best Local Similarity 1.3%; Score 26; DB 17; Length 808;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 680 TTTGAAGCTAAGTTGCTGATTTGG 705

## RESULT 7

US-10-425-114-1922  
; Sequence 1922, Application US/10425114  
; Publication No. US20040034888A1  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E  
; APPLICANT: Tabaska, Jack E  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
; FILE REFERENCE: 38-21(53313)B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 1922  
; LENGTH: 951  
; TYPE: DNA  
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US-10-425-114-1922

Query Match  
Best Local Similarity 1.3%; Score 26; DB 16; Length 951;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 16 TTTGAAGCTAAGTTGCTGATTTGG 41

## RESULT 8

US-10-425-114-13131  
; Sequence 13131, Application US/10425114  
; Publication No. US20040034888A1  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E  
; APPLICANT: Tabaska, Jack E  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
; FILE REFERENCE: 38-21(53313)B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 13131  
; LENGTH: 1011  
; TYPE: DNA  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: JC-GMFL02220096D10\_FLI  
US-10-425-114-13131

Query Match  
Best Local Similarity 1.3%; Score 26; DB 16; Length 1011;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1360 GAGAACTGACGTTTTCATTTGG 1385  
DB 246 GAGAACTGACGTTTTCATTTGG 271

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RESULT 9
US-10-425-115-143424
; Sequence 143424, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 143424
; LENGTH: 1100
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_6227C.1
US-10-425-115-143424

Query Match
Best Local Similarity 1.3%; Score 26; DB 16; Length 1100;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1231 TTGAAGCTAAGTTGCTGATTTGG 1256
DB 222 TTGAAGCTAAGTTGCTGATTTGG 247

RESULT 10
US-10-425-114-36420
; Sequence 36420, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 36420
; LENGTH: 1134
; TYPE: DNA
; ORGANISM: Zea mays subsp. mexicana
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMKOTEOSINTE097B02_FLI
US-10-425-114-36420

Query Match
Best Local Similarity 1.3%; Score 26; DB 16; Length 1134;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1231 TTGAAGCTAAGTTGCTGATTTGG 1256
DB 260 TTGAAGCTAAGTTGCTGATTTGG 285

RESULT 11
US-10-425-114-6300
; Sequence 6300, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua

; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 47702
; LENGTH: 1552
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_143080C.1
US-10-424-599-47702

Query Match
Best Local Similarity 1.3%; Score 26; DB 16; Length 1552;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1360 GAGAAGTCTGACGTTTCTCATTTGG 1385
DB 779 GAGAAGTCTGACGTTTCTCATTTGG 804

RESULT 12
US-10-424-599-47702
; Sequence 47702, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 47702
; LENGTH: 1552
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_143080C.1
US-10-424-599-47702

Query Match
Best Local Similarity 1.3%; Score 26; DB 16; Length 1500;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1360 GAGAAGTCTGACGTTTCTCATTTGG 1385
DB 779 GAGAAGTCTGACGTTTCTCATTTGG 804

RESULT 13
US-10-425-114-2326
; Sequence 2326, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
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; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 2326
; LENGTH: 1724
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700209610_FLI
US-10-425-114-2326

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Query Match          1.3%; Score 26; DB 16; Length 1724;
Best Local Similarity 100.0%; Pred. No. 0.0047;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1231 TTGAAGCTAAGTTGCTGATTTTG 1256
Db      832 TTGAAGCTAAGTTGCTGATTTTG 857

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RESULT 14
US-10-425-115-57011
; Sequence 57011, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 57011
; LENGTH: 2886
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_151984C.1
US-10-425-115-57011

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Query Match          1.3%; Score 26; DB 18; Length 2886;
Best Local Similarity 100.0%; Pred. No. 0.0047;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1231 TTGAAGCTAAGTTGCTGATTTTG 1256
Db      1886 TTGAAGCTAAGTTGCTGATTTTG 1911

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RESULT 15
US-10-425-115-72287
; Sequence 72287, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 72287
; LENGTH: 682
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure

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; LOCATION: (1)..(682)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_165926C.1
US-10-425-115-72287

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Query Match          1.3%; Score 25; DB 18; Length 682;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      669 ACCCTCTCCACCTCCACCAACGCGCT 693
Db      391 ACCCTCTCCACCTCCACCAACGCGCT 415

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Search completed: November 13, 2004, 17:11:15
Job time : 727 secs

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C 99	23	1.2	489	2	AM982145	AM982145 SSS00075 S	C 172	22	1.1	565	2	AM753578	AM753578
C 100	23	1.2	498	2	AM454236	AM454236 BR230015A	C 173	22	1.1	574	7	CF416485	CF416485
C 101	23	1.2	502	4	BG369831	BG369831 HVSME1002	C 174	22	1.1	591	6	CF023990	CF023990
C 102	23	1.2	515	2	AM418529	AM418529 x332c08.x	C 175	22	1.1	597	1	AJ453318	AJ453318
C 103	23	1.2	516	5	BU288421	BU288421 603604609	C 176	22	1.1	617	6	CB883350	CB883350
C 104	23	1.2	522	1	A1729561	A1729561 BNLGH1136	C 177	22	1.1	629	9	CL193146	CL193146
C 105	23	1.2	525	4	BG448469	BG448469 NF036E04R	C 178	22	1.1	632	9	CF415989	CF415989
C 106	23	1.2	529	4	BE637850	BE637850 WHE1755-1	C 179	22	1.1	633	7	CF839242	CF839242
C 107	23	1.2	530	1	AV554582	AV554582 AY554582	C 180	22	1.1	636	7	CF839242	CF839242
C 108	23	1.2	531	6	CA393582	CA393582 c839h10.y	C 181	22	1.1	648	8	BH022712	BH022712
C 109	23	1.2	534	2	AM375080	AM375080 QV1-CT011	C 182	22	1.1	667	5	BQ407542	BQ407542
C 110	23	1.2	534	6	CA233016	CA233016 SCGRUP306	C 183	22	1.1	676	1	AJ455502	AJ455502
C 111	23	1.2	535	6	CD922858	CD922858 G750.105F	C 184	22	1.1	677	6	CA927407	CA927407
C 112	23	1.2	542	5	BO316487	BO316487 QV1-CT011	C 185	22	1.1	680	1	AJ454164	AJ454164
C 113	23	1.2	550	2	AM134475	AM134475 UI-H-BT1-	C 186	22	1.1	685	7	CF809983	CF809983
C 114	23	1.2	567	5	BQ315895	BQ315895 QV1-CT011	C 187	22	1.1	690	1	AJ446992	AJ446992
C 115	23	1.2	572	2	BF042118	BF042118 BP250021B	C 188	22	1.1	691	6	CA237152	CA237152
C 116	23	1.2	573	4	BM815391	BM815391 EST593485	C 189	22	1.1	694	9	CL172776	CL172776
C 117	23	1.2	575	5	BI786430	BI786430 sa149a07.	C 190	22	1.1	698	8	BZ524377	BZ524377
C 118	23	1.2	578	5	BO316490	BO316490 QV1-CT011	C 191	22	1.1	705	9	CG069019	CG069019
C 119	23	1.2	585	1	AI1999650	AI1999650 701555869	C 192	22	1.1	707	7	CO046736	CO046736
C 120	23	1.2	594	5	BP131083	BP131083 BP131083	C 193	22	1.1	714	9	CG069020	CG069020
C 121	23	1.2	596	1	AV832259	AV832259 AV832259	C 194	22	1.1	718	7	CF415958	CF415958
C 122	23	1.2	596	2	AM617255	AM617255 EST323666	C 195	22	1.1	731	1	AJ448495	AJ448495
C 123	23	1.2	596	6	BO316492	BO316492 QV1-CT011	C 196	22	1.1	735	1	AJ445542	AJ445542
C 124	23	1.2	597	6	CA215962	CA215962 SCSEFL401	C 197	22	1.1	740	8	BH690594	BH690594
C 125	23	1.2	608	2	AM033109	AM033109 EST276668	C 198	22	1.1	741	8	BH550760	BH550760
C 126	23	1.2	608	4	BM814985	BM814985 EST593079	C 199	22	1.1	743	1	AJ451397	AJ451397
C 127	23	1.2	610	6	CA223791	CA223791 SCJFL1C0	C 200	22	1.1	756	8	CC387007	CC387007
C 128	23	1.2	611	6	CA237156	CA237156 SCMCFL500	C 201	22	1.1	760	1	AJ454727	AJ454727
C 129	23	1.2	618	1	AV826648	AV826648 AV826648	C 202	22	1.1	801	1	AJ446803	AJ446803
C 130	23	1.2	628	1	BI067795	BI067795 PG51n.pk0	C 203	22	1.1	855	9	CG036507	CG036507
C 131	23	1.2	628	4	BI067795	BI067795 PG51n.pk0	C 204	22	1.1	855	9	CG036507	CG036507
C 132	23	1.2	646	8	BH480820	BH480820 BOHLZ45TF	C 205	22	1.1	895	9	CG046981	CG046981
C 133	23	1.2	669	6	CA247444	CA247444 SCCCF1505	C 206	22	1.1	935	5	BX416490	BX416490
C 134	23	1.2	674	6	CA298046	CA298046 SCMCFL802	C 207	22	1.1	983	8	BZ465289	BZ465289
C 135	23	1.2	695	5	CA072174	CA072174 SCCCAM100	C 208	22	1.1	1020	8	BZ465289	BZ465289
C 136	23	1.2	696	9	CE670069	CE670069 LtGT-GRS-	C 209	22	1.1	124	2	BF586774	BF586774
C 137	23	1.2	697	6	CA066727	CA066727 SCJFLA101	C 210	22	1.1	242	4	BI178502	BI178502
C 138	23	1.2	700	8	BH550441	BH550441 BOHMF72TF	C 211	22	1.1	270	2	BB552920	BB552920
C 139	23	1.2	710	1	A1302817	A1302817 qm58h01.x	C 212	22	1.1	271	2	BE921790	BE921790
C 140	23	1.2	715	5	BU099573	BU099573 WHE3309 A	C 213	22	1.1	330	5	BU672062	BU672062
C 141	23	1.2	724	8	BH569945	BH569945 BOHHE60TR	C 214	22	1.1	341	7	CF860127	CF860127
C 142	23	1.2	729	8	BH982856	BH982856 odf13f09.	C 215	22	1.1	341	7	CO720101	CO720101
C 143	23	1.2	731	6	CB655196	CB655196 OSJNEC08F	C 216	22	1.1	370	1	AI154035	AI154035
C 144	23	1.2	736	5	BU595386	BU595386 AGENCOURT	C 217	22	1.1	370	7	CN577574	CN577574
C 145	23	1.2	745	1	AJ452950	AJ452950 AJ452950	C 218	22	1.1	373	5	EX303069	EX303069
C 146	23	1.2	750	5	BU302060	BU302060 603739336	C 219	22	1.1	382	1	CD231397	CD231397
C 147	23	1.2	764	1	AJ395192	AJ395192 AJ395192	C 220	22	1.1	382	1	AI486438	AI486438
C 148	23	1.2	765	5	BU240528	BU240528 603321372	C 221	22	1.1	390	7	CN041640	CN041640
C 149	23	1.2	781	7	CN793280	CN793280 4128280 B	C 222	22	1.1	392	7	CK460812	CK460812
C 150	23	1.2	782	5	BU354003	BU354003 603528486	C 223	22	1.1	395	6	BO300863	BO300863
C 151	23	1.2	786	8	BZ069046	BZ069046 1K36T01.	C 224	22	1.1	402	4	CD300863	CD300863
C 152	23	1.2	792	8	BH601781	BH601781 BOHRD80TR	C 225	22	1.1	404	7	CN035445	CN035445
C 153	23	1.2	811	7	CN232862	CN232862 WLA054E11	C 226	22	1.1	405	7	CN037599	CN037599
C 154	23	1.2	825	7	CN242228	CN242228 WLA054E11	C 227	22	1.1	407	7	RO2717	RO2717
C 155	23	1.2	865	7	CK205169	CK205169 FGAS01370	C 228	22	1.1	409	7	RO2717	RO2717
C 156	23	1.2	872	6	CA268425	CA268425 SCOSRT305	C 229	22	1.1	411	7	BE436813	BE436813
C 157	23	1.2	933	3	AM982539	AM982539 HVSME900	C 230	22	1.1	413	7	BE436813	BE436813
C 158	23	1.2	955	9	AG079376	AG079376 Pan.tlog1	C 231	22	1.1	413	7	BE436813	BE436813
C 159	23	1.2	1009	6	CA252912	CA252912 SCBFF1114	C 232	22	1.1	416	1	AA325689	AA325689
C 160	23	1.2	1114	6	CA278955	CA278955 SCBFF1109	C 233	22	1.1	422	6	CD847034	CD847034
C 161	23	1.2	1114	6	CA278955	CA278955 SCBFF1109	C 234	22	1.1	424	5	BO916616	BO916616
C 162	23	1.2	1257	8	BZ675184	BZ675184 PUBHE87TD	C 235	22	1.1	424	6	CB064470	CB064470
C 163	23	1.2	1276	1	AV008495	AV008495 AV008495	C 236	22	1.1	424	6	CB064470	CB064470
C 164	23	1.2	1416	5	BP652725	BP652725 BP652725	C 237	22	1.1	451	7	CN045547	CN045547
C 165	23	1.2	1433	5	AV791845	AV791845 AV791845	C 238	22	1.1	457	6	CD210897	CD210897
C 166	23	1.2	1490	4	BM358085	BM358085 GA_Ea000	C 239	22	1.1	458	7	RE5533	RE5533
C 167	23	1.2	1499	4	CD733903	CD733903 4046928 1	C 240	22	1.1	459	1	AJ249221	AJ249221
C 168	23	1.2	1524	6	CF799817	CF799817 Lt_PARCFC	C 241	22	1.1	459	6	AG225635	AG225635
C 169	23	1.2	1529	7	BZ620930	BZ620930 1966h07.B	C 242	22	1.1	459	6	AG225635	AG225635
C 170	23	1.2	1557	8	BZ620930	BZ620930 1966h07.B	C 243	22	1.1	459	6	AG225635	AG225635

C 244	21	1.1	461	7	CN038230	nm_26_b9	317	21	1.1	725	7	CN358608	CN358608 170005999
C 245	21	1.1	462	7	CN037727	rm_23_k6	C 318	21	1.1	739	6	CD285334	CD285334 G39164.86
C 246	21	1.1	465	7	CN042020	nm_36h_j2	C 319	21	1.1	741	4	BI936018	BI936018 EST555907
C 247	21	1.1	465	7	CN469507	hh_1b_Bra	C 320	21	1.1	746	3	CN509218	BN039234 Single re
C 248	21	1.1	470	7	CN036285	nm_14_15	C 321	21	1.1	751	7	CK720191	CK720191 20574 SWO
C 249	21	1.1	483	5	BO618122	fa56d10	C 322	21	1.1	753	8	BZ636310	BZ636310 OGAM5847C
C 250	21	1.1	483	7	CN043940	nm_22.2_d	C 323	21	1.1	754	3	CN509217	BN039234 Single re
C 251	21	1.1	483	7	R53242	Y966d12.t1	C 324	21	1.1	755	7	CG078179	CG078179 GR_Ba0P
C 252	21	1.1	494	1	AI771280	EST522296	C 325	21	1.1	757	8	BZ636313	BZ636313 OGAM5847M
C 253	21	1.1	494	4	BG447806	NE103A08E	C 326	21	1.1	770	5	BP753955	BP753955 BP753955
C 254	21	1.1	500	5	BQ262101	EST70H01.Y	C 327	21	1.1	774	5	EX863535	EX863535 EX863535
C 255	21	1.1	504	7	CK452686	908335_MA	C 328	21	1.1	777	7	CK720267	CK720267 20668 SWO
C 256	21	1.1	504	7	CK453752	909487_MA	C 329	21	1.1	778	9	CN5042M4	AL712669 Tetraodon
C 257	21	1.1	505	7	CN037461	nm_22.2_d	C 330	21	1.1	787	9	AG529449	AG529449 Mus muscu
C 258	21	1.1	505	7	W86386	zh55d06.t1	C 331	21	1.1	795	4	BI935482	BI935482 EST555371
C 259	21	1.1	506	7	CN040216	nm_35h_d8	C 332	21	1.1	804	4	BI753284	BI753284 60302615
C 260	21	1.1	510	7	CN038799	nm_29_110	C 333	21	1.1	806	3	CN509637	BN039234 Single re
C 261	21	1.1	511	5	CK460107	93035E_MA	C 334	21	1.1	807	9	CC739159	CC739159 ZMBMB010
C 262	21	1.1	515	5	CR348709	MediCa90	C 335	21	1.1	813	4	BG257479	BG257479 602377619
C 263	21	1.1	516	9	CR348709	MediCa90	C 336	21	1.1	813	4	BG545818	BG545818 602573096
C 264	21	1.1	526	6	CD060102	MA1-0006G	C 337	21	1.1	813	8	CC118014	CC118014 ND.L.20021
C 265	21	1.1	531	7	AL702099	DKFZP668B	C 338	21	1.1	827	9	CC733843	CC733843 OGKA697H
C 266	21	1.1	534	7	CK306048	1j99G01.Y	C 339	21	1.1	828	6	CA473587	CA473587 AGENCOURT
C 267	21	1.1	536	7	CN044440	v11_P51.h	C 340	21	1.1	835	9	CG925944	CG925944 MBEM1177R
C 268	21	1.1	539	6	CR210498	OML00778	C 341	21	1.1	844	9	CG226899	CG226899 OGXB6177H
C 269	21	1.1	542	8	BH882334	hw36906.b	C 342	21	1.1	847	7	CO806421	CO806421 AGENCOURT
C 270	21	1.1	545	5	BQ267225	1j99G01.Y	C 343	21	1.1	850	5	BO797643	BO797643 EST_6581
C 271	21	1.1	545	5	AW933703	EST359546	C 344	21	1.1	863	9	CL207367	CL207367 ZMBMB055
C 272	21	1.1	555	1	AI896248	EST265691	C 345	21	1.1	892	4	BG193644	BG193644 RST12778
C 273	21	1.1	557	2	BI847496	469344_MA	C 346	21	1.1	903	9	CG312007	CG312007 OG1CL94TV
C 274	21	1.1	561	2	AM655748	106986_MA	C 347	21	1.1	914	9	CG268102	CG268102 OGXDMS1TV
C 275	21	1.1	562	5	BQ263817	Iaai18d11	C 348	21	1.1	920	7	CK244611	CK244611 EST728248
C 276	21	1.1	564	8	BZ626373	1h45d09.b	C 349	21	1.1	921	3	CR705904	CR705904 Tetraodon
C 277	21	1.1	565	1	AU261086	AU261086	C 350	21	1.1	926	5	BX409971	BX409971 BX409971
C 278	21	1.1	579	4	BM380272	MEST517-F	C 351	21	1.1	933	7	CK254592	CK254592 EST738229
C 279	21	1.1	583	5	BU079690	946146F03	C 352	21	1.1	947	7	BT748877	BT748877 CH3#024_A
C 280	21	1.1	589	7	CN042561	v11_P43.b	C 353	21	1.1	947	7	CN020825	CN020825 AGENCOURT
C 281	21	1.1	591	2	BP242782	601877666	C 354	21	1.1	948	7	CK246533	CK246533 EST730170
C 282	21	1.1	594	2	BX306879	BX306879	C 355	21	1.1	964	8	CC426175	CC426175 PUHOA04TD
C 283	21	1.1	595	1	AI801887	AI801887	C 356	21	1.1	967	4	BM466173	BM466173 AGENCOURT
C 284	21	1.1	597	5	BP135468	BP135468	C 357	21	1.1	997	3	CN5099H4	BN058772 Single re
C 285	21	1.1	599	2	BO875889	BO875889	C 358	21	1.1	999	4	CK251691	CK251691 EST735328
C 286	21	1.1	602	6	CR847727	602079681	C 359	21	1.1	1015	9	BM469078	BM469078 AGENCOURT
C 287	21	1.1	603	6	CD846661	EST411923	C 360	21	1.1	1024	3	CN509HH3	BX058773 Single re
C 288	21	1.1	605	2	BE573288	602079681	C 361	21	1.1	1067	9	CN506OYO	AI411286 t3 end of
C 289	21	1.1	606	3	CR714685	CR714685	C 362	21	1.1	1127	5	BO067073	BO067073 AGENCOURT
C 290	21	1.1	609	7	CF858767	CF858767	C 363	21	1.1	1135	9	AT413691	AT413691 Homo sapi
C 291	21	1.1	609	7	CR714685	CR714685	C 364	21	1.1	1359	9	AT413692	AT413692 Pan trogl
C 292	21	1.1	616	7	CN045792	v11_P58.a	C 365	21	1.1	1365	9	AT413692	AT413692 Pan trogl
C 293	21	1.1	619	4	BG389914	602414105	C 366	21	1.1	1413	3	CR692038	CR692038 Tetraodon
C 294	21	1.1	622	6	CR831327	1117018E0	C 367	21	1.1	1423	9	CL493616	CL493616 SAIL_581
C 295	21	1.1	627	6	CA523309	KS12020H0	C 368	21	1.1	1433	3	CR687873	CR687873 Tetraodon
C 296	21	1.1	629	5	BU624937	UI-H-FG1	C 369	21	1.1	1437	3	CR686868	CR686868 Tetraodon
C 297	21	1.1	629	7	CN040661	nm_37h_j8	C 370	21	1.1	1444	3	CR692070	CR692070 Tetraodon
C 298	21	1.1	637	5	BO408233	GA_Ed000	C 371	21	1.1	1456	3	CR729013	CR729013 Tetraodon
C 299	21	1.1	639	4	BI178518	EST519463	C 372	21	1.1	1456	3	CN50A1NN	BN039234 Single re
C 300	21	1.1	640	5	BQ408325	GA_Ed001	C 373	21	1.1	1555	3	CN509Z04	ARABIDOPS
C 301	21	1.1	641	5	BQ409216	GA_Ed001	C 374	21	1.1	2041	3	CR615699	CR615699 full-length
C 302	21	1.1	646	5	BO390080	NISC mg11	C 375	21	1.0	2151	3	BR737616	BR737616 PM1-KT003
C 303	21	1.1	655	6	CD828414	BN25_070K	C 376	21	1.0	141	2	AT131553	AT131553
C 304	21	1.1	665	5	BU575172	PA_Ea000	C 377	21	1.0	141	2	CC053712	CC053712 SALK_0470
C 305	21	1.1	666	5	BO416196	GA_Ed010	C 378	21	1.0	169	8	AG529449	AG529449 Mus muscu
C 306	21	1.1	666	8	AO329920	nbXb0045P	C 379	21	1.0	179	1	BO904735	BO904735 Taq4_06h1
C 307	21	1.1	669	3	CNS09630	Single re	C 380	21	1.0	200	7	CN851169	CN851169 001001AIF
C 308	21	1.1	674	6	CD837334	BN45_051N	C 381	21	1.0	200	7	D40842	D40842
C 309	21	1.1	677	8	BH998130	oeF97b01	C 382	21	1.0	204	4	BZ683398	BZ683398
C 310	21	1.1	680	7	CNS47578	EST_16856	C 383	21	1.0	210	9	CG343415	CG343415
C 311	21	1.1	683	4	BJ307836	BU307836	C 384	21	1.0	213	1	AI254819	AI254819
C 312	21	1.1	702	4	BI922743	EST542647	C 385	21	1.0	215	7	D40889	D40889
C 313	21	1.1	712	4	CO074694	GR_Ea340	C 386	21	1.0	215	8	AZ310248	AZ310248
C 314	21	1.1	718	4	BM407268	EST581595	C 387	21	1.0	216	7	D40962	D40962
C 315	21	1.1	719	5	BM407268	EST581595	C 388	21	1.0	220	7	CN490249	CN490249
C 316	21	1.1	719	7	CF571601	MC5015G05	C 389	21	1.0	223	5	BP746939	BP746939



C 390	20	1.0	226	2	AM268259	xx34e07.x	C 463	20	1.0	442	2	BF933983	BF933983	IL5-NT022
C 391	20	1.0	226	6	C97797	Rice	C 464	20	1.0	443	1	AUI62019	AUI62019	ARI62019
C 392	20	1.0	226	6	AM985398	NNV 134	C 465	20	1.0	445	9	CRI67302	CRI67302	Reverse s
C 393	20	1.0	228	6	C28342	Rice	C 466	20	1.0	448	2	BE850718	BE850718	UI-M-ML1
C 394	20	1.0	228	1	AJ602547		C 467	20	1.0	448	6	CD730608	CD730608	4038937 1
C 395	20	1.0	246	2	BB376598		C 468	20	1.0	449	6	CB742885	CB742885	AMGNNUC:N
C 396	20	1.0	259	2	BE127071	DEPA0820	C 469	20	1.0	453	6	CA021495	CA021495	H240E08
C 397	20	1.0	250	4	BU696352	Bj696352	C 470	20	1.0	454	5	BO973693	BO973693	QH113401
C 398	20	1.0	256	6	CA715674	wk33c.pk0	C 471	20	1.0	457	6	CA693279	CA693279	wlm96.pk0
C 399	20	1.0	261	7	CF449068	EST685413	C 472	20	1.0	459	7	CN604794	CN604794	USDA.FP.1
C 400	20	1.0	272	2	BB404901		C 473	20	1.0	462	1	AU070018	AU070018	AU070018
C 401	20	1.0	272	5	BU882397	UM761E05	C 474	20	1.0	466	4	BG673922	BG673922	MINM53.WI
C 402	20	1.0	294	6	CD451406	USDA-FP.1	C 475	20	1.0	467	1	AU094366	AU094366	AU094366
C 403	20	1.0	296	8	BH229564	1006153A1	C 476	20	1.0	467	6	CF076930	CF076930	QHR14C05
C 404	20	1.0	303	6	CD711874	VVC025B05	C 477	20	1.0	471	1	AU082232	AU082232	AU082232
C 405	20	1.0	304	6	C28596		C 478	20	1.0	471	6	CB009693	CB009693	VND004F08
C 406	20	1.0	309	2	BB164234		C 479	20	1.0	471	6	CB911950	CB911950	VND137H12
C 407	20	1.0	314	1	AV156120		C 480	20	1.0	474	1	A1527911	A1527911	vj30E07.Y
C 408	20	1.0	324	6	CA358644	631400.NC	C 481	20	1.0	475	8	BH230076	BH230076	1006155H0
C 409	20	1.0	328	6	CA686747	wlm96.pk0	C 482	20	1.0	478	4	BG591632	BG591632	EST499474
C 410	20	1.0	331	6	CD711358		C 483	20	1.0	483	5	BO995886	BO995886	OCG11B09
C 411	20	1.0	332	5	BY103114	BY103114	C 484	20	1.0	487	6	CD668301	CD668301	gec1c.pk0
C 412	20	1.0	333	6	CD191126	MS1-0068T	C 485	20	1.0	480	9	CG408876	CG408876	De570.Ds
C 413	20	1.0	335	1	AU069458		C 486	20	1.0	492	1	AU395325	AU395325	AU395325
C 414	20	1.0	343	6	CB322164	EST0282.M	C 487	20	1.0	492	2	BE435261	BE435261	EST406339
C 415	20	1.0	344	2	AM269298		C 488	20	1.0	493	4	B1338401	B1338401	362166.MA
C 416	20	1.0	345	6	CA517485	K509081C0	C 489	20	1.0	494	7	CN768392	CN768392	lat66E04
C 417	20	1.0	345	9	CR087542	Forward.s	C 490	20	1.0	497	7	CN744093	CN744093	SAL.US027
C 418	20	1.0	349	1	AU163327		C 491	20	1.0	499	1	AUI61382	AUI61382	AUI61382
C 419	20	1.0	353	2	AW326743		C 492	20	1.0	503	2	BF642076	BF642076	NR031P051
C 420	20	1.0	353	6	CB914070	VVD008D10	C 493	20	1.0	508	1	A1992665	A1992665	701498357
C 421	20	1.0	355	1	AU069451		C 494	20	1.0	508	4	BM136347	BM136347	WHR2608.G
C 422	20	1.0	358	2	BF321858	uz65d10.Y	C 495	20	1.0	510	2	AM751828	AM751828	QV1-CT011
C 423	20	1.0	353	8	BY035468		C 496	20	1.0	510	2	B1797955	B1797955	H092P07.E
C 424	20	1.0	365	5	AZ134878		C 497	20	1.0	515	9	CE815919	CE815919	Liqr-GSS-
C 425	20	1.0	373	7	CO779500		C 498	20	1.0	515	9	CG934620	CG934620	MBRD107TR
C 426	20	1.0	374	6	CA029117	H264E01r	C 499	20	1.0	519	2	BE439917	BE439917	HTWL-S32F
C 427	20	1.0	376	7	D41252		C 500	20	1.0	522	1	AL921277	AL921277	AL921277
C 428	20	1.0	378	5	BX835823		C 501	20	1.0	522	6	CD883972	CD883972	FL.115A05
C 429	20	1.0	380	4	BG649500	EMI.80.B0	C 502	20	1.0	526	7	CF910684	CF910684	AO603C07-
C 430	20	1.0	380	4	B1750890		C 503	20	1.0	527	1	AU298769	AU298769	AU298769
C 431	20	1.0	380	8	BH229752	Ta01.02g1	C 504	20	1.0	527	6	CA655334	CA655334	wlm0.pk00
C 432	20	1.0	381	2	AM428824	Lj1tmpst	C 505	20	1.0	529	6	CB910568	CB910568	VVD152B04
C 433	20	1.0	381	2	BB842445	BB842445	C 506	20	1.0	529	6	CA661382	CA661382	wlmk1.pk0
C 434	20	1.0	382	1	AU069318		C 507	20	1.0	531	6	CB718981	CB718981	AMGNNUC:C
C 435	20	1.0	383	5	BX836728		C 508	20	1.0	531	7	CN904918	CN904918	OL0926ABD
C 436	20	1.0	385	5	BP095881		C 509	20	1.0	534	5	BU866680	BU866680	M11BH02.P
C 437	20	1.0	388	2	AM685205	NFC02612N	C 510	20	1.0	534	6	CD475087	CD475087	na033-12M
C 438	20	1.0	389	1	AJ440591		C 511	20	1.0	536	4	BG909189	BG909189	Ta01.174H
C 439	20	1.0	392	2	BE116010	UI-R-B81-	C 512	20	1.0	537	7	CF656134	CF656134	ta054E07.
C 440	20	1.0	398	1	AU069368		C 513	20	1.0	537	7	CF656134	CF656134	ta054E07.
C 441	20	1.0	398	6	C97625		C 514	20	1.0	537	7	CK626526	CK626526	m23a08.Y
C 442	20	1.0	400	7	CO070313		C 515	20	1.0	541	6	CD547847	CD547847	B0283C07-
C 443	20	1.0	401	1	AV540214		C 516	20	1.0	542	1	AUI61185	AUI61185	AUI61185
C 444	20	1.0	402	4	BG096869	EST461388	C 517	20	1.0	542	7	CK934402	CK934402	CGF100425
C 445	20	1.0	402	6	CA002462		C 518	20	1.0	543	5	BQ567640	BQ567640	g193h03.Y
C 446	20	1.0	404	7	D43598		C 519	20	1.0	544	1	A1896155	A1896155	EST265598
C 447	20	1.0	404	5	BO122054	EST607630	C 520	20	1.0	546	6	CB876723	CB876723	HP02D02T
C 448	20	1.0	409	6	CD213095	H51.28.G0	C 521	20	1.0	547	8	BM029055	BM029055	RPCT-24-2
C 449	20	1.0	409	1	AUI61252		C 522	20	1.0	549	6	CB922232	CB922232	VVD081B08
C 450	20	1.0	409	5	BO583881	EO11887-0	C 523	20	1.0	549	6	CD474696	CD474696	na003-12M
C 451	20	1.0	412	2	BE847002		C 524	20	1.0	550	5	BX523315	BX523315	BX523315
C 452	20	1.0	413	1	A1120709	uw72a06.r	C 525	20	1.0	553	6	CB3122416	CB3122416	UI-R-DY0-
C 453	20	1.0	419	2	BE946554	UI-M-BH3-	C 526	20	1.0	556	1	AA592307	AA592307	vo23a08.r
C 454	20	1.0	428	6	CA628059	w1c1.pk00	C 527	20	1.0	559	5	BU481445	BU481445	G18.106K
C 455	20	1.0	429	7	CA744746	w1c1c.pk0	C 528	20	1.0	559	5	CD887952	CD887952	G18.106K
C 456	20	1.0	429	7	CO541092		C 529	20	1.0	562	5	BU977465	BU977465	HAL1H16r
C 457	20	1.0	434	1	AL911110		C 530	20	1.0	562	6	CB922795	CB922795	rvd008A12
C 458	20	1.0	434	6	CA692661	wlm96.pk0	C 531	20	1.0	562	6	B1863136	B1863136	tm6h07.Y
C 459	20	1.0	435	8	BH307919		C 532	20	1.0	568	7	CF912178	CF912178	A0627E09-
C 460	20	1.0	440	2	BE293896		C 533	20	1.0	569	7	CG907920	CG907920	Ta01.163G
C 461	20	1.0	441	2	BE192914		C 534	20	1.0	571	3	CNS08EXU	CNS08EXU	Single re
C 462	20	1.0	441	8	AQ816045	HS_5437_B	C 535	20	1.0	571	3	CNS08EXU	CNS08EXU	Single re

C 536	20	1.0	571	6	CA654848	CA654848	wlmo.pk00	609	20	1.0	658	7	CN847503	CN847503	FG07042B0
C 537	20	1.0	571	8	BZ249089	BZ249089	CH230-261	C 610	20	1.0	659	2	BE216915	BE216915	EST0458 T
C 538	20	1.0	575	5	CB008231	CB008231	VVC05C06	C 611	20	1.0	660	8	AZ570798	AZ570798	278PvH01
C 539	20	1.0	578	4	BI473662	BI473662	fp40d12.y	C 612	20	1.0	663	8	BZ512063	BZ512063	BOMR214TR
C 540	20	1.0	578	6	CA659125	CA659125	wlm1.pk00	C 613	20	1.0	664	4	BI305444	BI305444	NLP_1.G18
C 541	20	1.0	578	6	CD890929	CD890929	GL18.115M	C 614	20	1.0	664	6	CB916243	CB916243	VVD108D03
C 542	20	1.0	578	9	CG018800	CG018800	ZADV46TV	C 615	20	1.0	665	1	AJ800922	AJ800922	AGJ000922
C 543	20	1.0	579	5	BO620385	BO620385	TALR1165F	C 616	20	1.0	667	6	CF211662	CF211662	AGJ000922
C 544	20	1.0	579	6	CD817416	CD817416	BN20.041N	C 617	20	1.0	667	6	CF211662	CF211662	AGJ000922
C 545	20	1.0	581	6	C99251	C99251	C99251.C99251.R1ce	C 618	20	1.0	668	6	CD862783	CD862783	T22A1TF TAM
C 546	20	1.0	581	7	CK767202	CK767202	wm101.7ms	C 619	20	1.0	669	6	CA817315	CA817315	CA12E1203
C 547	20	1.0	581	7	CA243486	CA243486	SCQ6FL407	C 620	20	1.0	670	7	CF723779	CF723779	UI-M-GZ0-
C 548	20	1.0	585	7	CF449761	CF449761	EST168106	C 621	20	1.0	671	7	CO070312	CO070312	GR_Ba27E
C 549	20	1.0	585	9	FR0048387	FR0048387	Fugu.rubr	C 622	20	1.0	672	2	AM133859	AM133859	fi12f07.y
C 550	20	1.0	588	5	BQ240853	BQ240853	TaB05012B	C 623	20	1.0	673	5	BO410602	BO410602	GA_Ed003
C 551	20	1.0	588	4	BX087108	BX087108	FX087108	C 624	20	1.0	674	5	BO804242	BO804242	WHE3552.B
C 552	20	1.0	589	4	BI721687	BI721687	NF011A11F	C 625	20	1.0	675	4	BI921202	BI921202	EST541105
C 553	20	1.0	593	4	BI243821	BI243821	BU243821	C 626	20	1.0	675	6	CA342846	CA342846	672802.NC
C 554	20	1.0	593	7	CB812988	CB812988	VVD160C02	C 627	20	1.0	675	6	CF744209	CF744209	UI-M-GV0-
C 555	20	1.0	594	6	CF913024	CF913024	A0641H07-	C 628	20	1.0	677	6	CB005720	CB005720	VVC025B05
C 556	20	1.0	594	7	CO783693	CO783693	BL018C.G0	C 629	20	1.0	681	3	CNS0817Y	CNS0817Y	single.re
C 557	20	1.0	599	5	BU045682	BU045682	PP_LBA002	C 630	20	1.0	682	6	CD890928	CD890928	single.re
C 558	20	1.0	599	7	CF777360	CF777360	ta09f08	C 631	20	1.0	686	5	BU039453	BU039453	PP_LBA000
C 559	20	1.0	606	5	BQ237794	BQ237794	TaB05012B	C 632	20	1.0	690	1	AI980300	AI980300	pac.pk002
C 560	20	1.0	607	1	AU094417	AU094417	AU094417	C 633	20	1.0	692	6	CD880613	CD880613	FI_075E21
C 561	20	1.0	607	6	CA676785	CA676785	wlm12.pk0	C 634	20	1.0	693	8	BH966736	BH966736	od127c11.
C 562	20	1.0	608	4	BM737493	BM737493	952056E05	C 635	20	1.0	694	9	AG301331	AG301331	Mus.muscu
C 563	20	1.0	610	6	CD875341	CD875341	AZ03.104N	C 636	20	1.0	695	4	BM064115	BM064115	KS01063C0
C 564	20	1.0	610	7	CF656442	CF656442	tac54e07.	C 637	20	1.0	695	7	CK949116	CK949116	4073966.B
C 565	20	1.0	612	4	BG573786	BG573786	602594877	C 638	20	1.0	696	4	BI955091	BI955091	HVSMEM02
C 566	20	1.0	613	6	CA682253	CA682253	wlm124.pk0	C 639	20	1.0	698	7	CK263600	CK263600	EST709678
C 567	20	1.0	613	6	CB916586	CB916586	VLD11D05	C 640	20	1.0	705	5	BO996505	BO996505	OGG31A10.
C 568	20	1.0	614	8	BZ650280	BZ650280	OGCAR277C	C 641	20	1.0	706	5	BX319785	BX319785	BX319785
C 569	20	1.0	617	8	CA070858	CA070858	SCUTAD103	C 642	20	1.0	706	7	CK215248	CK215248	FGAS02720
C 570	20	1.0	618	6	CA269355	CA269355	SCBGR307	C 643	20	1.0	706	8	BH423283	BH423283	BOH0407R
C 571	20	1.0	620	6	CA759582	CA759582	BR060005B	C 644	20	1.0	706	8	BH393836	BH393836	odf03f12.
C 572	20	1.0	620	6	CA759583	CA759583	BR060007B	C 645	20	1.0	707	6	CB340294	CB340294	CA23E102I
C 573	20	1.0	620	5	CB578941	CB578941	AMGNNUC:N	C 646	20	1.0	708	8	BE601936	BE601936	HVSMEM10.
C 574	20	1.0	621	5	BU994363	BU994363	HM06M12F	C 647	20	1.0	708	2	BZ375959	BZ375959	ie63e12.g
C 575	20	1.0	623	4	CF777103	CF777103	ta09f08	C 648	20	1.0	710	7	CF576349	CF576349	MCSA179A0
C 576	20	1.0	624	4	BM003510	BM003510	1031111A0	C 649	20	1.0	710	8	BH117090	BH117090	RPT-24.3
C 577	20	1.0	625	4	BM878778	BM878778	PI6-C03.S	C 650	20	1.0	710	8	BH952227	BH952227	odh91a12.
C 578	20	1.0	625	9	CNS0401Z	CNS0401Z	Tetraodon	C 651	20	1.0	712	6	BE585781	BE585781	Est#1pT7
C 579	20	1.0	630	9	CF413663	CF413663	SCSCS027B	C 652	20	1.0	712	6	CF213190	CF213190	CGF100063
C 580	20	1.0	631	6	CD618039	CD618039	55114091J	C 653	20	1.0	713	6	CF232896	CF232896	PCATX0001
C 581	20	1.0	632	7	CN880366	CN880366	010417AAS	C 654	20	1.0	715	5	BO863251	BO863251	OGC23G04.
C 582	20	1.0	633	8	AO920598	AO920598	RPT-23-2	C 655	20	1.0	717	2	AM175049	AM175049	fi13f12.y
C 583	20	1.0	634	5	BQ259329	BQ259329	fz97h09.y	C 656	20	1.0	718	2	AM203151	AM203151	fj10d04.x
C 584	20	1.0	636	6	CF213117	CF213117	CGF100063	C 657	20	1.0	722	7	CO536181	CO536181	ta112h05.
C 585	20	1.0	636	5	CN881117	CN881117	010425AAS	C 658	20	1.0	723	9	CG269706	CG269706	OGABT10TC
C 586	20	1.0	638	5	BX645283	BX645283	DKFP781P	C 659	20	1.0	724	7	CK315956	CK315956	SB02028B1
C 587	20	1.0	639	5	CD873491	CD873491	AZ03.000H	C 660	20	1.0	724	8	BZ057547	BZ057547	1k9754a09.
C 588	20	1.0	640	6	CA596906	CA596906	wp1c.pk0	C 661	20	1.0	725	6	CA815406	CA815406	CA12E1203
C 589	20	1.0	642	1	AI6588024	AI6588024	fc22d12.y	C 662	20	1.0	725	6	CA817834	CA817834	CA12E1301
C 590	20	1.0	644	5	BO998850	BO998850	QGG20G20.	C 663	20	1.0	728	7	CF800440	CF800440	MIM325.M
C 591	20	1.0	645	2	BE213667	BE213667	EST0357.T	C 664	20	1.0	731	9	CNS03MAJ	CNS03MAJ	Tetraodon
C 592	20	1.0	645	2	BE213674	BE213674	EST0365.T	C 665	20	1.0	733	1	AJ794246	AJ794246	CA12E1203
C 593	20	1.0	646	5	CD876127	CD876127	AZ03.108K	C 666	20	1.0	733	6	CA815916	CA815916	CA12E1301
C 594	20	1.0	646	6	CD874312	CD874312	AZ03.101N	C 667	20	1.0	737	7	CF2318057	CF2318057	FGAS03006
C 595	20	1.0	649	6	CD894445	CD894445	GL18.126E	C 668	20	1.0	739	6	CF231837	CF231837	PLaC0026D
C 596	20	1.0	651	1	AU239156	AU239156	AU239156	C 669	20	1.0	742	9	CNS042BQ	CNS042BQ	AT771403
C 597	20	1.0	651	6	CD862014	CD862014	AZ01.102A	C 670	20	1.0	745	4	BS309101	BS309101	HVSMEMC00
C 598	20	1.0	651	6	CF211757	CF211757	CGF100066	C 671	20	1.0	746	4	BS672070	BS672070	DRNCBF02
C 599	20	1.0	651	7	CN943923	CN943923	010928AVB	C 672	20	1.0	754	4	BS671728	BS671728	DRNBX11TH
C 600	20	1.0	652	6	CB914612	CB914612	VVD012H05	C 673	20	1.0	755	9	CC605217	CC605217	OGMBU11TH
C 601	20	1.0	653	4	BU567885	BU567885	BU567885	C 674	20	1.0	756	5	BU004395	BU004395	OGG5B11.y
C 602	20	1.0	654	2	BE213532	BE213532	EST0222.T	C 675	20	1.0	756	5	CNS03WNF	CNS03WNF	AT639400
C 603	20	1.0	654	5	BX629100	BX629100	BX629100	C 676	20	1.0	760	7	CK215872	CK215872	FGA020784
C 604	20	1.0	654	6	CB557548	CB557548	AMGNNUC:N	C 677	20	1.0	761	7	CK215684	CK215684	FGA020765
C 605	20	1.0	654	7	CN941498	CN941498	010918AVB	C 678	20	1.0	761	9	BX996523	BX996523	Reverse.S
C 606	20	1.0	657	8	AZ570929	AZ570929	280PvE03	C 679	20	1.0	763	6	CA368745	CA368745	645005.NC
C 607	20	1.0	658	8	CD876742	CD876742	AZ03.110M	C 680	20	1.0	765	5	BX861013	BX861013	BX861013
C 608	20	1.0	658	7	CP913260	CP913260	A0645H03-	C 681	20	1.0	770	9	CG327586	CG327586	OGMJF82TV

682	20	1.0	771	8	AQ869176	nbeb0034E	755	20	1.0	967	8	CC387004	CC387004	PUIHP31TB
683	20	1.0	772	9	CC844186	NDL..8703.	756	20	1.0	967	9	CG396708	CG396708	ZMMB8C001
684	20	1.0	773	4	BG446509	GA..EB003	757	20	1.0	970	9	CG832404	CG832404	ZMMB8C012
685	20	1.0	774	4	BT733904		758	20	1.0	969	9	CL047856	CL047856	CH216-66P
686	20	1.0	774	7	CK772723		759	20	1.0	993	9	CNS04E4G	CNS04E4G	
687	20	1.0	775	5	BX869090	BX869090	760	20	1.0	994	9	CNS0364G	CNS0364G	
688	20	1.0	775	7	CN204870	Tor5256 G	761	20	1.0	1006	9	CNS020BQ	CNS020BQ	
689	20	1.0	777	7	CN203296	Tor3546 G	762	20	1.0	1009	9	CNS08EXV	CNS08EXV	
690	20	1.0	779	6	CB595784		763	20	1.0	1009	9	CNS03B30	CNS03B30	
691	20	1.0	779	6	CNS03JTB		764	20	1.0	1010	9	CNS08RCR	CNS08RCR	
692	20	1.0	785	5	AG303553		765	20	1.0	1028	9	CNS04LFO	CNS04LFO	
693	20	1.0	787	5	BX643868	Mus muscu	766	20	1.0	1035	4	BM471782	BM471782	
694	20	1.0	787	6	CD353587	UI-M-GM0-	767	20	1.0	1052	3	CNS08SW7	CNS08SW7	
695	20	1.0	796	7	CK255367	EST753004	768	20	1.0	1054	3	CNS08SM6	CNS08SM6	
696	20	1.0	798	7	CNS34460	UI-M-HS0-	769	20	1.0	1075	7	CK216031	CK216031	
697	20	1.0	798	9	CC757010	ZMMB8B014	770	20	1.0	1086	7	CK212338	CK212338	
698	20	1.0	801	7	CF448808	EST685153	771	20	1.0	1104	7	CK212338	CK212338	
699	20	1.0	803	2	BF617530	HVSM8C001	772	20	1.0	1165	5	BQ481514	BQ481514	
700	20	1.0	804	6	CA387503	669490 NC	773	20	1.0	1165	9	CL647240	CL647240	
701	20	1.0	805	8	A2126212	OSJNB007	774	20	1.0	1199	7	CK211542	CK211542	
702	20	1.0	809	4	BM020213	603648802	775	20	1.0	1239	5	BQ433478	BQ433478	
703	20	1.0	811	9	CC923999	LO72114ba	776	20	1.0	1330	8	CC252781	CC252781	
704	20	1.0	813	7	CNS29912	UI-M-HQ0-	777	20	1.0	1377	3	CR729663	CR729663	
705	20	1.0	813	9	CC972005	ZUHP07TH	778	20	1.0	1381	2	BE917283	BE917283	
706	20	1.0	818	6	CB976208	CA840001	779	20	1.0	1393	3	BG181131	BG181131	
707	20	1.0	819	8	CK257469	EST741106	780	20	1.0	1439	3	CR730285	CR730285	
708	20	1.0	819	8	CK130181	NDL..8703.	781	20	1.0	1466	3	CR727014	CR727014	
709	20	1.0	821	4	BG369396	HVSM8C002	782	20	1.0	1558	2	BF343362	BF343362	
710	20	1.0	821	6	CB288850	V-B-19G08	783	20	1.0	1579	2	CNS0A70T	CNS0A70T	
711	20	1.0	821	6	BZ492400	BONQD32TR	784	20	1.0	1713	2	BF237925	BF237925	
712	20	1.0	825	4	BT731966	603355828	785	20	1.0	2396	3	AK085066	AK085066	
713	20	1.0	826	6	CB76623	CA820006	786	20	1.0	3061	3	AK045502	AK045502	
714	20	1.0	833	6	CB976130	CA840002	787	20	1.0	3070	3	AK034476	AK034476	
715	20	1.0	839	5	BU294050	603604977	788	20	1.0	3681	3	AK082191	AK082191	
716	20	1.0	841	7	CK194594	FGAS00302	789	19	1.0	129	4	BI430830	BI430830	
717	20	1.0	844	9	CG256899	OG0DU65TV	790	19	1.0	140	6	CB403622	CB403622	
718	20	1.0	850	9	B2190372	CH230-378	791	19	1.0	141	2	BE592936	BE592936	
719	20	1.0	851	6	CB976869	CA840003	792	19	1.0	153	5	BU003721	BU003721	
720	20	1.0	851	6	CL514687	SAITL..892-	793	19	1.0	151	8	AZ592680	AZ592680	
721	20	1.0	858	7	CP616776	AGENCOURT	794	19	1.0	185	5	BU005495	BU005495	
722	20	1.0	866	8	AZ558244	RPCT-23-2	795	19	1.0	198	9	CL624395	CL624395	
723	20	1.0	866	8	BH468052	BOHOU24TF	796	19	1.0	199	8	BH697244	BH697244	
724	20	1.0	867	4	BG682141	602629436	797	19	1.0	200	8	BH146119	BH146119	
725	20	1.0	867	9	CG302905	OG0CC58TH	798	19	1.0	202	1	AV344438	AV344438	
726	20	1.0	870	5	BU557303	AGENCOURT	799	19	1.0	205	9	CNS07HAC	CNS07HAC	
727	20	1.0	876	9	CNS026JC		800	19	1.0	216	8	AZ072472	AZ072472	
728	20	1.0	882	4	BG196646	RST15872	801	19	1.0	218	7	D39814	D39814	
729	20	1.0	882	9	CC981689	ZDACT64TH	802	19	1.0	218	9	CR217060	CR217060	
730	20	1.0	884	5	BQ715449	AGENCOURT	803	19	1.0	219	6	CB403255	CB403255	
731	20	1.0	885	9	CNS01VOL		804	19	1.0	225	5	BQ867189	BQ867189	
732	20	1.0	891	9	CG417256	B2454381	805	19	1.0	225	7	CN204931	CN204931	
733	20	1.0	893	8	BZ454381	BONKX80TR	806	19	1.0	227	9	CE607770	CE607770	
734	20	1.0	894	9	CG089355	PUCVCY9TD	807	19	1.0	228	2	BM597730	BM597730	
735	20	1.0	898	4	B1154955	602902760	808	19	1.0	232	1	AV113701	AV113701	
736	20	1.0	906	8	BZ755102	PUREF10TD	809	19	1.0	233	1	AJ770492	AJ770492	
737	20	1.0	907	9	CC718705	OGUHU3JTH	810	19	1.0	234	1	AA494656	AA494656	
738	20	1.0	911	9	CR201007	Forward s	811	19	1.0	236	7	D39872	D39872	
739	20	1.0	921	9	CNS02ATK		812	19	1.0	238	9	CE027689	CE027689	
740	20	1.0	927	6	CB558023	AGENCOURT	813	19	1.0	239	8	AZ100984	AZ100984	
741	20	1.0	930	4	BG676499	602622960	814	19	1.0	240	1	AA824186	AA824186	
742	20	1.0	934	7	CK290232	EST752946	815	19	1.0	242	1	AA896507	AA896507	
743	20	1.0	936	4	B1948363	HVSM8C000	816	19	1.0	242	2	AW214731	AW214731	
744	20	1.0	936	4	B2149448	HV..CEB000	817	19	1.0	243	9	CR115916	CR115916	
745	20	1.0	938	3	CNS08RCO	Single re	818	19	1.0	249	9	CN873860	CN873860	
746	20	1.0	943	9	CG327577	OGMUF82TH	819	19	1.0	251	5	BQ965597	BQ965597	
747	20	1.0	943	9	CC353901	POHEBD9TD	820	19	1.0	252	7	CD085307	CD085307	
748	20	1.0	946	8	BUI47813	AGENCOURT	821	19	1.0	258	6	CD060143	CD060143	
749	20	1.0	953	8	BH156460	ENTFS63TR	822	19	1.0	264	6	CD450544	CD450544	
750	20	1.0	954	8	BZ755100	PUREF10TB	823	19	1.0	269	9	CL206131	CL206131	
751	20	1.0	955	2	BE418203	SCU022.FO	824	19	1.0	270	2	BE584984	BE584984	
752	20	1.0	961	9	CNS03Q95		825	19	1.0	270	6	CA999795	CA999795	
753	20	1.0	965	3	CNS08L7Z	Single re	826	19	1.0	272	1	AV113791	AV113791	
754	20	1.0					827	19	1.0					

C 828	19	1.0	275	6	CA700199	CA700199	WkMlc.pK0	C 901	19	1.0	339	6	CF327086	CF327086	NACL--01-
C 829	19	1.0	275	7	CK766222	CK766222	ltu01-13m	C 902	19	1.0	341	7	CF645659	CF645659	K39_A04 F
C 830	19	1.0	275	7	CN851191	CN851191	001001AAE	C 903	19	1.0	341	7	D46796	D46796	RtCS11694A
C 831	19	1.0	276	2	BB158036	BB158036	BB158036	C 904	19	1.0	341	9	CR037812	CR037812	Reverse s
C 832	19	1.0	276	9	CB466241	CB466241	ltgr-gss-	C 905	19	1.0	344	1	AV544699	AV544699	AV544699
C 833	19	1.0	278	8	BH171185	BH171185	SALK_0039	C 906	19	1.0	344	6	CB833114	CB833114	USDA-PP 1
C 834	19	1.0	280	1	AV080506	AV080506	AV080506	C 907	19	1.0	347	1	AV216352	AV216352	AV216352
C 835	19	1.0	280	1	AV156324	AV156324	AV156324	C 908	19	1.0	348	6	CF074822	CF074822	AV216352
C 836	19	1.0	282	2	BH424168	BH424168	WHE0076_A	C 909	19	1.0	348	6	CF076877	CF076877	QHR13M06
C 837	19	1.0	285	1	AJ772432	AJ772432	AJ772432	C 910	19	1.0	348	6	CG727954	CG727954	1139097D0
C 838	19	1.0	285	1	AJ772771	AJ772771	AJ772771	C 911	19	1.0	349	6	CF089765	CF089765	OHM23021
C 839	19	1.0	285	1	AV133589	AV133589	AV133589	C 912	19	1.0	349	7	CN875476	CN875476	010204AAR
C 840	19	1.0	286	1	AJ772364	AJ772364	AB054448	C 913	19	1.0	353	7	CN851230	CN851230	001002AAE
C 841	19	1.0	286	2	BB054448	BB054448	BB054448	C 914	19	1.0	356	5	BQ912459	BQ912459	QHA20M13
C 842	19	1.0	286	8	BZ666396	BZ666396	SGT5680-3	C 915	19	1.0	360	8	AZ794535	AZ794535	2M0048B22
C 843	19	1.0	288	1	AV061868	AV061868	AV061868	C 916	19	1.0	361	1	AV736618	AV736618	AV736618
C 844	19	1.0	288	6	CB213488	CB213488	OML03768	C 917	19	1.0	361	2	BP345545	BP345545	602019116
C 845	19	1.0	288	7	CF850710	CF850710	PSMA015XJ	C 918	19	1.0	361	2	BP802363	BP802363	CMO-CT009
C 846	19	1.0	289	1	AV137010	AV137010	AV137010	C 919	19	1.0	361	6	CD490043	CD490043	TJ1_H04 T
C 847	19	1.0	289	1	AV522187	AV522187	AV522187	C 920	19	1.0	361	6	CN656678	CN656678	rt40a01.Y
C 848	19	1.0	289	1	AV563133	AV563133	AV563133	C 921	19	1.0	362	6	CD489215	CD489215	T20_C06 T
C 849	19	1.0	291	5	BY390277	BY390277	BY390277	C 922	19	1.0	365	7	CN860889	CN860889	000823AAF
C 850	19	1.0	292	1	AV010867	AV010867	AV010867	C 923	19	1.0	366	6	BY665030	BY665030	BY665030
C 851	19	1.0	293	4	BI038285	BI038285	RCS-NTD26	C 924	19	1.0	367	4	BI129871	BI129871	G096P70Y
C 852	19	1.0	294	1	AI165524	AI165524	A08SP15u	C 925	19	1.0	368	2	AW706671	AW706671	sk01d05.Y
C 853	19	1.0	295	1	AV145218	AV145218	AV145218	C 926	19	1.0	368	6	CF091067	CF091067	QHM6P14.Y
C 854	19	1.0	295	2	BE444977	BE444977	WHE1130_G	C 927	19	1.0	369	2	AW705601	AW705601	sk50b06.Y
C 855	19	1.0	295	4	BI315914	BI315914	saf65a014	C 928	19	1.0	369	7	CF644697	CF644697	K24_D03 F
C 856	19	1.0	295	8	AZ615809	AZ615809	1M0445014	C 929	19	1.0	369	8	BH229102	BH229102	1061150B0
C 857	19	1.0	297	5	BO860233	BO860233	OGC15D06	C 930	19	1.0	370	1	AI594531	AI594531	vc05f04.Y
C 858	19	1.0	297	5	BU236117	BU236117	603408522	C 931	19	1.0	370	2	BF907354	BF907354	MRO-UT004
C 859	19	1.0	300	1	AV008370	AV008370	AV008370	C 932	19	1.0	370	5	BY422279	BY422279	BY422279
C 860	19	1.0	300	6	CS6252	CS6252	CS6252	C 933	19	1.0	372	6	CA756828	CA756828	OC11D11_T
C 861	19	1.0	300	6	CS6970	CS6970	CS6970	C 934	19	1.0	373	1	AA024235	AA024235	m10b12.X
C 862	19	1.0	300	6	CS8261	CS8261	CS8261	C 935	19	1.0	374	4	BI319223	BI319223	949027B09
C 863	19	1.0	300	6	CS9261	CS9261	CS9261	C 936	19	1.0	374	9	CG827207	CG827207	ZMBB0031
C 864	19	1.0	300	7	D45986	D45986	RtCS10319A	C 937	19	1.0	375	7	T67258	T67258	y453901.r4
C 865	19	1.0	302	9	CG645207	CG645207	OST389492	C 938	19	1.0	376	4	BU249018	BU249018	BU249018
C 866	19	1.0	305	2	BE930748	BE930748	RC1-GN007	C 939	19	1.0	380	9	CE532315	CE532315	ltgr-gss-
C 867	19	1.0	305	7	DA0833	DA0833	RtCS2996A_R	C 940	19	1.0	381	6	CA938619	CA938619	sav35d60
C 868	19	1.0	305	8	AZ358393	AZ358393	1M0100113	C 941	19	1.0	382	2	BE526981	BE526981	602070260
C 869	19	1.0	306	1	AA590789	AA590789	ym21c12.r	C 942	19	1.0	382	8	BH229147	BH229147	1061150D1
C 870	19	1.0	306	6	CA004168	CA004168	HSMBB047	C 943	19	1.0	383	1	AA615556	AA615556	vc09c03.T
C 871	19	1.0	308	6	AA823689	AA823689	vm37g01.r	C 944	19	1.0	383	7	CK632397	CK632397	AM1-AP000
C 872	19	1.0	311	1	BE594222	BE594222	WS1_103_G	C 945	19	1.0	384	2	BE426870	BE426870	QHE19F21
C 873	19	1.0	312	2	AA981902	AA981902	ua3db11.r	C 946	19	1.0	384	5	BU018681	BU018681	QHE19F21
C 874	19	1.0	313	7	CN849284	CN849284	000901AAE	C 947	19	1.0	384	8	BH229134	BH229134	1006150D0
C 875	19	1.0	313	8	BH916412	BH916412	3526_1_52	C 948	19	1.0	385	2	BE661484	BE661484	402_GmaxS
C 876	19	1.0	315	4	BU086847	BU086847	CF643297	C 949	19	1.0	386	2	AM451554	AM451554	UT-H-BI3-
C 877	19	1.0	315	7	CF643297	CF643297	D65_B03_F	C 950	19	1.0	386	6	CD490277	CD490277	T35_D05 T
C 878	19	1.0	316	5	BO869588	BO869588	OGF6U23_Y	C 951	19	1.0	386	6	CE759605	CE759605	ltgr-gss-
C 879	19	1.0	316	8	BZ733444	BZ733444	OGF6U51TC	C 952	19	1.0	387	2	AM747173	AM747173	WS1_66_E0
C 880	19	1.0	317	6	CB857388	CB857388	DH0XG19ZB	C 953	19	1.0	387	5	BY934876	BY934876	BY934876
C 881	19	1.0	317	6	BI130639	BI130639	G108P61Y	C 954	19	1.0	387	5	CH074125	CH074125	EST01756
C 882	19	1.0	319	4	AV014053	AV014053	AV014053	C 955	19	1.0	387	6	FR0031119	FR0031119	Fuga_rubr
C 883	19	1.0	321	6	CA507600	CA507600	UI-R-FS1-	C 956	19	1.0	387	9	BC241718	BC241718	RH122_50
C 884	19	1.0	322	6	CF327085	CF327085	NACL--01-	C 957	19	1.0	389	4	CN428776	CN428776	170006001
C 885	19	1.0	322	6	CG240392	CG240392	OVI_29_E0	C 958	19	1.0	394	7	AX920294	AX920294	Reverse s
C 886	19	1.0	323	4	AZ454483	AZ454483	1M0257G06	C 959	19	1.0	394	9	CI260348	CI260348	ZMBB0061
C 887	19	1.0	324	8	BU493583	BU493583	NO_ADGR_D	C 960	19	1.0	394	9	CG089121	CG089121	ut68C06.Y
C 888	19	1.0	325	5	BE205987	BE205987	BB205987	C 961	19	1.0	395	4	BE089121	BE089121	1008054H0
C 889	19	1.0	331	2	CK099811	CK099811	A085P15_5	C 962	19	1.0	395	8	AA693246	AA693246	vr58e09.s
C 890	19	1.0	326	7	AA608804	AA608804	af04e06_s	C 963	19	1.0	397	5	BQ265893	BQ265893	NISC_f09
C 891	19	1.0	326	4	BO640361	BO640361	RST43051	C 964	19	1.0	397	8	AO028925	AO028925	CIT-HSP-2
C 892	19	1.0	326	5	BO667214	BO667214	OGD10C02	C 965	19	1.0	397	5	AT037401	AT037401	ub52c10.r
C 893	19	1.0	331	2	BE609955	BE609955	NXST_053_	C 966	19	1.0	398	1	CF293278	CF293278	30DGS--02
C 894	19	1.0	331	2	BE205987	BE205987	BB205987	C 967	19	1.0	398	7	CO786011	CO786011	NT003A_BI
C 895	19	1.0	331	2	CA640962	CA640962	wreln.pK0	C 968	19	1.0	399	7	CA524576	CA524576	KS1204D00
C 896	19	1.0	332	6	CO786803	CO786803	BL287B_E1	C 969	19	1.0	400	6	CA933857	CA933857	MTU03T5_P1
C 897	19	1.0	332	7	TS3901	TS3901	YB83e10_F1	C 970	19	1.0	400	6	CA933936	CA933936	MTU03T5_P1
C 898	19	1.0	333	7	BE609943	BE609943	NXST_047	C 971	19	1.0	400	6	BE228417	BE228417	As_Lgz_27
C 899	19	1.0	333	7	CN861408	CN861408	001012AAG	C 972	19	1.0	401	2	AZ462586	AZ462586	1M02691L9
C 900	19	1.0	338	7				C 973	19	1.0	402	8			

## ALIGNMENTS

membership trench program in plant genomics

co.intobrogen.tr).

Mismatches 2; Indels 0; Gaps 0;

ATGTCATGTAGATGACAGCTTAGTTGACTGGGACCA 1473

551 AATGGGAAGATTAAGAGAACCGTTCAGGGCTAATAGTGGACCTTCTCTTTAA 601

**DEFINITION** BOGLN68:IK BOGL Brassica oleracea genomic clone BOGLN68, genomic

SOURCE Brassica oleracea

JOURNAL  
Unpublished (2001)  
04-1-2001

## FEATURES

/note="vector; site\_1: BstXI; 2-3 kb sheared"

ORIGIN

Query Match 14.0%; Score 273; DB 8; Length 453;  
Best Local Similarity 100.0%; Pred. No. 1.3e-131;  
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1627 CAGATTGGCGTGGTTGAGAGAAATGATCATCTGTCAGATCTTAAAGAAAGGATGAGA 1686  
DB 169 CAGATTGGCGTGGTTGAGAGAAATGATCATCTGTCAGATCTTAAAGAAAGGATGAGA 228

QY 1687 CCAGGTCAAGCATGTATACAGCTCATAGGAGAAACCCGATTATGATCGAGCCAG 1746  
DB 229 CCAGGTCAAGCATGTATACAGCTCATAGGAGAAACCCGATTATGATCGAGCCAG 288

QY 1747 TACATGAAGCATGATGAAGATTAGGAAATGCGACCTTGGAATCAAGATACAGCC 1806  
DB 289 TACATGAAGCATGATGAAGATTAGGAAATGCGACCTTGGAATCAAGATACAGCC 348

QY 1807 ACGGGTGAATACGATTAATCCGACGATGACTATGACTGTACCCGTCTGTTCAAGCAGC 1866  
DB 349 ACGGGTGAATACGATTAATCCGACGATGACTATGACTGTACCCGTCTGTTCAAGCAGC 408

QY 1867 GAGGGCCAAACACACCGGAAATGAGATGGGG 1899  
DB 409 GAGGGCCAAACACACCGGAAATGAGATGGGG 441

RESULT 3  
BZ455058 753 bp DNA linear GSS 13-DEC-2002  
LOCUS BOKNA33TF.B0.1.6\_2\_KB.tot Brassica oleracea genomic clone BOKNA33,  
DEFINITION genomic survey sequence.  
ACCESSION BZ455058  
VERSION BZ455058.1 GI:26731783  
KEYWORDS GSS.

SOURCE  
ORGANISM  
Brassica oleracea  
Brassica oleracea  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.  
1 (bases 1 to 753)  
Town, C.D., Van Aken, S., Uterback, T., Koo, H. and Fraser, C.M.  
Whole genome shotgun sequencing of Brassica oleracea  
Unpublished (2001)  
Other GSSs: BOKNA33TF  
Contact: Chris Town  
TIGR  
9712 Medical Center Drive, Rockville, MD 20850, USA.  
Tel: 301-838-3523  
Fax: 301-838-0208  
Email: cdtown@tigr.org  
DNA is from a doubled haploid provided by Tom Osborn.  
Seq primer: TP  
Class: sheared ends.

FEATURES  
source  
1..753  
Location/Qualifiers  
/organism="Brassica oleracea"  
/mol\_type="Genomic DNA"  
/strain="TO1000DH3"  
/db\_xref="taxon:3712"  
/clone="BOKNA33"  
/clone\_1id="BO.1.6\_2\_KB.tot"  
/note="Vector: pHOSt1, Site 1: BstXI; 1.6-2 kb sheared  
total DNA inserted into pHOSt1 using BstXI linkers"

ORIGIN

Query Match 9.6%; Score 187; DB 8; Length 753;  
Best Local Similarity 100.0%; Pred. No. 2.5e-86;  
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1282 AACACGATGTATCAACAGCTGTGATGGAACTTTGGTACTTGGCTCCGGAATACGCT 1341  
DB 11 AACACGATGTATCAACAGCTGTGATGGAACTTTGGTACTTGGCTCCGGAATACGCT 70

QY 1342 GCAAGCGAAAAGCTCACGGAGAGTCTGACGTTTCTCATTTGGCGTTGGAG 1401  
DB 71 GCAAGCGAAAAGCTCACGGAGAGTCTGACGTTTCTCATTTGGCGTTGGAG 130

QY 1402 CTCTATTCTGGAGGTGACCCCGTTGATGCCAACAATCTTATGATGACAGTTAGT 1461  
DB 131 CTCTATTCTGGAGGTGACCCCGTTGATGCCAACAATCTTATGATGACAGTTAGT 190

QY 1462 GACTGGG 1468  
DB 191 GACTGGG 197

RESULT 4  
BX834233/c 853 bp mRNA linear EST 11-FEB-2004  
LOCUS BX834233  
DEFINITION BX834233 Arabidopsis thaliana Adult vegetative tissue Col-0  
Arabidopsis thaliana cDNA clone GSLTLS22ZF07 3PRIM, mRNA sequence.  
ACCESSION BX834233  
VERSION BX834233.1 GI:42517711  
KEYWORDS EST.

SOURCE  
ORGANISM  
Arabidopsis thaliana (thale cress)  
Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
1 (bases 1 to 853)  
Castelli, V., Aubry, J.M., Jallion, O., Wincker, P., Clepet, C.,  
Menard, M., Cruaud, C., Quetier, F., Scarpetelli, C., Schachter, V.,  
Temple, G., Caboche, M., Weissenbach, J. and Salanoubat, M.  
Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences:  
A Combined Approach to Evaluate and Improve Arabidopsis Genome  
Annotation  
Unpublished (2004)

JOURNAL  
COMMENT  
Genoscope - Centre National de Sequencage  
BP 191 91006 EVRY cedex - France  
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
The sequences are based on single pass reads.  
Life Technologies (a division of Invitrogen) members carried out  
full-length libraries construction : Temple G.  
Genoscope members carried out sequencing and annotation : Castelli  
V., Aubry J.M., Jallion O., Wincker P., Menard M., Cruaud C.,  
Schachter V., Weissenbach J., Salanoubat M.  
URGV INRA : Clepet C., Caboche M.  
Annotation is based on the June 2003 version of the Arabidopsis  
genome released by MIPS (Munich Information center for Protein  
Sequences).  
http://www.genoscope.cns.fr/externe/sequences/Banque\_Projet\_EF/EST  
http://www.genoscope.cns.fr/cgi-bin/gdb/gdb?source=Arabidopsis.

FEATURES  
source  
1..853  
Location/Qualifiers  
/organism="Arabidopsis thaliana"  
/mol\_type="mRNA"  
/ecotype="Col-0"  
/db\_xref="taxon:3702"  
/clone="GSLTLS22ZF07"  
/tissue\_type="Adult vegetative tissue"  
/clone\_1id="Arabidopsis thaliana Adult vegetative tissue  
Col-0"

ORIGIN

Query Match 3.4%; Score 66; DB 5; Length 853;  
Best Local Similarity 100.0%; Pred. No. 1.2e-22;  
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1432 AACATGTCTATGTGATGACAGCTTACTGATCGGACACACATTCCTTAACCGACA 1491  
DB 668 AACATGTCTATGTGATGACAGCTTACTGATCGGACACACATTCCTTAACCGACA 609

QY 1492 TCTGAG 1497  
DB 11 TCTGAG 1497

Db 608 TCTGAG 603

RESULT 5  
LOCUS CNS0440X  
DEFINITION Arabidopsis thaliana Full-length cDNA Complete sequence from clone GS115712E12 of Adult vegetative tissue of strain col-0 of Arabidopsis thaliana (thale cress).  
ACCESSION BX823746.1 GI:42462388  
VERSION HTG; GSUT cDNA.  
SOURCE Arabidopsis thaliana (thale cress)  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eustosids II; Brassicales; Brassicaceae; Arabidopsis.  
1 (bases 1 to 2106)  
Castelli,V., Aury,J.M., Jallion,O., Wincker,P., Clepet,C., Menard,M., Cruaud,C., Quetier,F., Scarpelli,C., Schachter,V., Temple,G., Caboche,M., Weissenbach,J. and Salanoubat,M.  
Whole Genome Sequence Comparisons and 'Full-length' cDNA Sequences:  
A Combined Approach to Evaluate and Improve Arabidopsis Genome Annotation  
Unpublished  
2 (bases 1 to 2106)  
Genoscope.  
Direct Submission  
Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqret@genoscope.cns.fr  
- Web : www.genoscope.cns.fr)  
The sequences are based on single pass reads.  
Life Technologies (a division of Invitrogen) members carried out full-length libraries construction : Temple G.  
Genoscope members carried out sequencing and annotation : Castelli V., Aury J.M., Jallion O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M.  
URGV INRA : Clepet C., Caboche M.  
Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences) . 5 prime and 3 prime are assembled with Phrap.  
http://www.genoscope.cns.fr/externe/sequences/Banque\_Projet\_EF/FullLength  
http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis.  
Location/Qualifiers  
1..2106  
/organism="Arabidopsis thaliana"  
/mol\_type="mRNA"  
/strain="Col-0"  
/db\_xref="taxon:3702"  
/clone="GS115712E12"  
/tissue\_type="Adult vegetative tissue"  
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1..2106  
/gene="At3g24550"

ORIGIN

Query Match 3.4%; Score 66; DB 3; Length 2106;  
Best Local Similarity 100.0%; Pred. No. 1.3e-22;  
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1432 AACAAATGCTATGTAGTACAGCTTATGTTACTGGGACGACCATTTGCTTAACCGAGCA 1491  
DB 1520 AACAAATGCTATGTAGTACAGCTTATGTTACTGGGACGACCATTTGCTTAACCGAGCA 1579  
QY 1492 TCTGAG 1497  
DB 1580 TCTGAG 1585

RESULT 6  
LOCUS CD811645  
DEFINITION

DEFINITION BN10.001E08F011207 BN10 Brassica napus cDNA clone BN10001E08, mRNA sequence.  
ACCESSION CD811645  
VERSION CD811645.1 GI:32493585  
KEYWORDS EST.  
SOURCE Brassica napus (rape)  
ORGANISM Brassica napus  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eustosids II; Brassicales; Brassicaceae; Brassica.  
1 (bases 1 to 314)  
Genoplatte.  
A major partnership french program in plant genomics  
Unpublished (2003)  
Contact: Genoplatte  
Genoplatte  
93, rue Henri Rochefort 91025 EVRY CEDEX France  
Tel: 33 1 69 47 54 00  
Fax: 33 1 69 47 54 10  
This sequence has been generated in the framework of the french plant genomics programme 'Genoplatte' (http://www.genoplatte.com and http://genoplatte-info.infobiogen.fr).  
Location/Qualifiers  
1..314  
/organism="Brassica napus"  
/mol\_type="mRNA"  
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/db\_xref="taxon:3708"  
/clone="BN10001E08"  
/tissue\_type="seed"  
/clone\_1ib="BN10"

ORIGIN

Query Match 3.3%; Score 65; DB 6; Length 314;  
Best Local Similarity 99.1%; Pred. No. 3.9e-22;  
Matches 115; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1825 CCGACCAATGCTATGACTGTACCCGCTCTGTTCAAGCAGGAGCCAAACCAACGCG 1884  
DB 1 CCGACCAATGCTATGACTGTACCCGCTCTGTTCAAGCAGGAGCCAAACCAACGCG 60  
QY 1885 GAAATGCAATGGGGAAGATTAGAGAACCGGTGAGGTTATAGTGAACCTTCTCT 1940  
DB 61 GAGATGCAATGGGGAAGATTAGAGAACCGGTGAGGTTATAGTGAACCTTCTCT 116

RESULT 7  
LOCUS CD811912  
DEFINITION CD811912 314 bp mRNA linear EST 10-JUL-2003  
BN10.01G03F020121 BN10 Brassica napus cDNA clone BN10019G03, mRNA sequence.  
ACCESSION CD811912  
VERSION CD811912.1 GI:32493852  
KEYWORDS EST.  
SOURCE Brassica napus (rape)  
ORGANISM Brassica napus  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eustosids II; Brassicales; Brassicaceae; Brassica.  
1 (bases 1 to 314)  
Genoplatte.  
A major partnership french program in plant genomics  
Unpublished (2003)  
Contact: Genoplatte  
Genoplatte  
93, rue Henri Rochefort 91025 EVRY CEDEX France  
Tel: 33 1 69 47 54 00  
Fax: 33 1 69 47 54 10  
This sequence has been generated in the framework of the french plant genomics programme 'Genoplatte' (http://www.genoplatte.com and http://genoplatte-info.infobiogen.fr).  
Location/Qualifiers  
1..314



ORIGIN

Query Match 3.3%; Score 65; DB 6; Length 314;  
Best Local Similarity 99.1%; Pred. No. 3.9e-22;  
Matches 115; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1825 CCGACGAGTACTATGACTGTACCGCTGTGTTCAAGCAGCGAGGCGCAACACACGCG 1884  
DB 1 CCGACGAGTACTATGACTGTACCGCTGTGTTCAAGCAGCGAGGCGCAACACACGCG 60

QY 1885 GAATGAGATGGGGAAGATTAGAGAACCGGTGAGGTTATATGACCTTCTCT 1940  
DB 61 GAGATGAGATGGGGAAGATTAGAGAACCGGTGAGGTTATATGACCTTCTCT 116

RESULT 8  
AV539333/c 561 bp mRNA linear EST 20-FEB-2004

LOCUS  
DEFINITION  
AV539333 Arabidopsis thaliana roots Columbia Arabidopsis thaliana  
CDNA clone R2130C07F 3', mRNA sequence.

ACCESSION  
AV539333

VERSION  
AV539333.1 GI:8701090

KEYWORDS  
EST

SOURCE  
Arabidopsis thaliana (thale cress)

ORGANISM  
Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
1 (bases 1 to 561)  
Asamizu, Y., Nakamura, Y., Sato, S. and Tabata, S.  
A large scale analysis of cDNA in Arabidopsis thaliana: Generation  
of 12,028 non-redundant expressed sequence tags from normalized and  
size-selected cDNA libraries  
DNA Res. 7 (3), 175-180 (2000)

JOURNAL  
MEDLINE  
PUBMED  
10907847

COMMENT  
Contact: Erika Asamizu  
The First Laboratory for Plant Gene Research  
Kazusa DNA Research Institute  
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan  
Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.  
Location/Qualifiers

FEATURES  
Source  
1. 561  
/organism="Arabidopsis thaliana"  
/mol\_type="mRNA"  
/ecotype="Columbia"  
/db\_xref="taxon:3702"  
/clone="R2130C07F"  
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/clone\_lib="Arabidopsis thaliana roots Columbia"  
/note="Vector: pBluescriptII SK-; Site\_1: EcoRI; Site\_2:  
XhoI"

ORIGIN

Query Match 2.7%; Score 53; DB 1; Length 561;  
Best Local Similarity 100.0%; Pred. No. 8.3e-16;  
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1579 GCTGCGGCTGTGTTGCCATTGAGCTCGCGGAGACCTGCGATGAGCCAGAT 1631  
DB 543 GCTGCGGCTGTGTTGCCATTGAGCTCGCGGAGACCTGCGATGAGCCAGAT 491

RESULT 9  
AV543493/c 584 bp mRNA linear EST 20-FEB-2004

LOCUS

DEFINITION  
AV543493 Arabidopsis thaliana roots Columbia Arabidopsis thaliana  
CDNA clone R2201F07F 3', mRNA sequence.

ACCESSION  
AV543493

VERSION  
AV543493.1 GI:8714907

KEYWORDS  
EST

SOURCE  
Arabidopsis thaliana (thale cress)

ORGANISM  
Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
1 (bases 1 to 584)  
Asamizu, Y., Nakamura, Y., Sato, S. and Tabata, S.  
A large scale analysis of cDNA in Arabidopsis thaliana: Generation  
of 12,028 non-redundant expressed sequence tags from normalized and  
size-selected cDNA libraries  
DNA Res. 7 (3), 175-180 (2000)

JOURNAL  
MEDLINE  
PUBMED  
10907847

COMMENT  
Contact: Erika Asamizu  
The First Laboratory for Plant Gene Research  
Kazusa DNA Research Institute  
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan  
Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.  
Location/Qualifiers

FEATURES  
Source  
1. 584  
/organism="Arabidopsis thaliana"  
/mol\_type="mRNA"  
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/db\_xref="taxon:3702"  
/clone="R2201F07F"  
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/clone\_lib="Arabidopsis thaliana roots Columbia"  
/note="Vector: pBluescriptII SK-; Site\_1: EcoRI; Site\_2:  
XhoI"

ORIGIN

Query Match 2.7%; Score 53; DB 1; Length 584;  
Best Local Similarity 100.0%; Pred. No. 8.3e-16;  
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1579 GCTGCGGCTGTGTTGCCATTGAGCTCGCGGAGACCTGCGATGAGCCAGAT 1631  
DB 468 GCTGCGGCTGTGTTGCCATTGAGCTCGCGGAGACCTGCGATGAGCCAGAT 416

RESULT 10  
BH432371 754 bp DNA linear GSS 12-DEC-2001

LOCUS  
BH432371  
BOGVQ937R BOGV Brassica oleracea genomic clone BOGVQ93, genomic  
survey sequence.

ACCESSION  
BH432371

VERSION  
BH432371.1 GI:17618092

KEYWORDS  
GSS

SOURCE  
Brassica oleracea

ORGANISM  
Brassica oleracea  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.  
1 (bases 1 to 754)  
Town, C.D., Van Aken, S., Uterback, T., Koo, H. and Fraser, C.M.  
Whole genome shotgun sequencing of Brassica oleracea  
Unpublished (2001)  
Other GSSs: BOGVQ937F  
Contact: Chris Town  
TIGR

REFERENCE  
9712 Medical Center Drive, Rockville, MD 20850, USA.  
Tel: 301-838-3523  
Fax: 301-838-0208  
Email: cdtown@tigr.org  
DNA is from a doubled haploid provided by Tom Osborn.  
Seq primer: TR  
Class: sheared ends.  
Location/Qualifiers

source 1. .754  
 /organism="Brassica oleracea"  
 /mol\_type="genomic DNA"  
 /strain="T01000DH3"  
 /db\_xref="taxon:3712"  
 /clone="BOGV93"  
 /note="Vector: PHOS1; Site 1: BstXI; 2-3 kb sheared genomic DNA inserted into PHOS1 using BstXI linkers"

ORIGIN

Query Match 2.2%; Score 42; DB 8; Length 754;  
 Best Local Similarity 100.0%; Pred. No. 5.2e-10;  
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1762 AAGAGTTTGGAAATGGCACTTGGAACTCAAGATCAAC 1803  
 |||||  
 462 AAGAGTTTGGAAATGGCACTTGGAACTCAAGATCAAC 503

RESULT 11  
 BZ456327 342 bp DNA linear GSS 13-DEC-2002  
 LOCUS B0NB666R BO\_1.6\_2\_KB\_tot Brassica oleracea genomic clone B0NB666,  
 DEFINITION genomic survey sequence.  
 ACCESSION BZ456327  
 VERSION BZ456327.1 GI:26734454  
 KEYWORDS GSS.  
 SOURCE Brassica oleracea  
 ORGANISM Brassica oleracea  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.  
 1 (bases 1 to 342)  
 Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.  
 Whole genome shotgun sequencing of Brassica oleracea  
 TITLE Unpublished (2001)  
 JOURNAL  
 COMMENT Contact: Chris Town  
 TIGR  
 9712 Medical Center Drive, Rockville, MD 20850, USA.  
 Tel: 301-838-3523  
 Fax: 301-838-0208  
 Email: cdtown@tigr.org  
 DNA is from a doubled haploid provided by Tom Osborn.  
 Seq primer: TR  
 Class: sheared ends.  
 Location/Qualifiers  
 1..342  
 /organism="Brassica oleracea"  
 /mol\_type="genomic DNA"  
 /strain="T01000DH3"  
 /db\_xref="taxon:3712"  
 /clone="B0NB666"  
 /clone\_1lb="BO\_1.6\_2\_KB\_tot"  
 /note="Vector: PHOS1; Site 1: BstXI; 1.6-2 kb sheared total DNA inserted into PHOS1 using BstXI linkers"

ORIGIN

Query Match 1.5%; Score 32; DB 8; Length 342;  
 Best Local Similarity 100.0%; Pred. No. 9.1e-05;  
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 CCATCTCCACCATCAACTCCACACACACAC 68  
 |||||  
 182 CCATCTCCACCATCAACTCCACACACACAC 213

RESULT 12  
 BZ066106 744 bp DNA linear GSS 10-OCT-2002  
 LOCUS BZ066106/c  
 DEFINITION 1j176e12.g1 B.oleracea002 Brassica oleracea genomic, genomic survey  
 sequence.  
 ACCESSION BZ066106

VERSION BZ066106.1 GI:23679353  
 KEYWORDS GSS.  
 SOURCE Brassica oleracea  
 ORGANISM Brassica oleracea  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.  
 1 (bases 1 to 744)  
 Delehaunty,K., Fewell,G., Fulton,L., McCombie,W.R., Miner,T.,  
 Nash,W., Rabinowicz,P.D. and Wilson,R.K.  
 Whole genome shotgun reads from Brassica oleracea  
 TITLE Unpublished (2002)  
 JOURNAL  
 COMMENT Contact: Richard K. Wilson  
 Genome Sequencing Center  
 Washington University School of Medicine  
 Email: submissions@watson.wustl.edu  
 Plate: 1j1770 row: e column: 12  
 Seq primer: -28RPOT reverse  
 Class: shotgun  
 High quality sequence start: 17  
 High quality sequence stop: 551.  
 Location/Qualifiers  
 1..744  
 /organism="Brassica oleracea"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:3712"  
 /clone\_1lb="B.oleracea002"  
 /note="Vector: POTW13; Whole genome shotgun library from  
 flowering buds. DNA was purified from a crude nuclear  
 prep using Brassica oleracea T01000DH3 buds provided by  
 Thomas Osborn at the University of Wisconsin. Genomic  
 DNA was provided by Pablo Rabinowicz (CSHL) and the  
 shotgun library prepared at Washington University Genome  
 Sequencing Center."

ORIGIN

Query Match 1.5%; Score 30; DB 8; Length 744;  
 Best Local Similarity 100.0%; Pred. No. 0.0011;  
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1596 CCATCAGCTCGCCGAGACCTCGCATGAG 1625  
 |||||  
 729 CCATCAGCTCGCCGAGACCTCGCATGAG 700

RESULT 13  
 CL469889/c 925 bp DNA linear GSS 01-APR-2004  
 LOCUS SA1L\_135\_B06.v1 SA1L Collection Arabidopsis thaliana genomic clone  
 DEFINITION SA1L\_135\_B06.v1, genomic survey sequence.  
 ACCESSION CL469889  
 VERSION CL469889.1 GI:45935600  
 KEYWORDS GSS.  
 SOURCE Arabidopsis thaliana (thale cress)  
 ORGANISM Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 1 (bases 1 to 925)  
 Sessions,A., Burke,B., Presting,G., Aux,G., McEliver,J., Paton,D.,  
 Dietrich,B., Ho,P., Bacwaden,J., Ko,C., Clarke,D., Cotton,D.,  
 Bullis,D., Snell,J., Miguel,T., Hutchinson,D., Kimerly,B.,  
 Mitzel,T., Katagiri,F., Glazebrook,J., Law,M. and Goff,S.A.  
 A high-throughput Arabidopsis reverse genetics system  
 TITLE Plant Cell 14 (12), 2985-2994 (2002)  
 JOURNAL  
 MEDLINE  
 PubMed  
 22356987  
 12468722  
 CONTACT: Sessions A  
 Applied Trait Genetics  
 Syngenta Biotechnology Inc.  
 3054 Cornwallis Rd., Research Triangle Park, NC 27709, USA  
 Email: allen.sessions@syngenta.com  
 ABRC Stock Number CS806541; T-DNA left border flanking sequences of

Syngenta Arabidopsis Insertion Library (SAIL) lines are available through the Arabidopsis Biological Resource Center (ABRC). Sequences represent a pool of amplified genomic regions and not single contiguous sequences.  
Class: TDNA tagged.

FEATURES  
source  
Location/Qualifiers  
1..925

/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/ecotype="Columbia"  
/db\_xref="taxon:3702"  
/clone="SAIL\_135\_B06\_v1"  
/note="T-DNA left border sequences were isolated using a modified TAIL-PCR strategy"

ORIGIN

Query Match 1.5%; Score 30; DB 9; Length 925;  
Best Local Similarity 100.0%; Pred. No. 0.0011;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1548 CAGAGAGAGATGGCTCGCATGTTGCTTG 1577  
121 CAGAGAGAGATGGCTCGCATGTTGCTTG 92

RESULT 14  
LOCUS C0066237 472 bp mRNA linear EST 15-JUN-2004  
DEFINITION Md2w2062j06.v1 Mdfw Matus x domestica cDNA clone Md2w2062j06.5' similar to TR:Q9ZN08 Q9ZN08 PUTATIVE SERINE/THREONINE PROTEIN KINASE.; mRNA sequence.

ACCESSION C0066237  
VERSION C0066237  
KEYWORDS  
SOURCE  
ORGANISM Matus x domestica (cultivated apple)

REFERENCE  
AUTHORS  
Aldwinckle, H., Malnoy, M., Carroll, N., Goldbrough, P., Orvis, K., Clifton, S., Page, D., Maita, M., Hillier, L., Martin, J., Wylie, T., Dante, M., Theising, B., Bowers, Y., Gibbons, M., Ritters, E., Ronko, I., Tsagaris, R., Kennedy, S., Waterson, R., and Wilson, R.  
1 (bases 1 to 472)  
Korban, S., Vokhlova, L., Liu, L., Gasic, K., Gonzales, O., Hernandez, A., Aldwinckle, H., Malnoy, M., Carroll, N., Goldbrough, P., Orvis, K., Clifton, S., Page, D., Maita, M., Hillier, L., Martin, J., Wylie, T., Dante, M., Theising, B., Bowers, Y., Gibbons, M., Ritters, E., Ronko, I., Tsagaris, R., Kennedy, S., Waterson, R., and Wilson, R.  
1 (bases 1 to 472)  
Apple Functional Genomics grant - NSF 0321702  
Unpublished (2004)

TITLE  
JOURNAL  
COMMENT  
Contact: Schuyler S. Korban  
Apple Functional Genomics grant - NSF 0321702  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
Library materials provided by: Schuyler S. Korban Library  
constructed by: A. Hernandez / K. Gasic Library sequenced by:  
Washington University Genome Sequencing Center  
Mashu EST name: aah50e03.v1  
Seq primer: -40UP from Gibco  
High quality sequence stop: 472.  
Location/Qualifiers  
1..472

FEATURES  
source  
/organism="Matus x domestica"  
/mol\_type="mRNA"  
/db\_xref="taxon:3750"  
/clone="Md2w2062j06"  
/lab\_host="DH10B ampicillin resistant"  
/clone\_lib="Mdfw"  
/note="Vector: DH10B ampicillin resistant; Site 1: NotI; Site 2: EcoRI; Total RNA was extracted separately from each stage (bud, balloon, open and after pollination) using the 'pine tree' method. Poly(A)+mRNA was isolated

twice from total RNA from each stage using the Oligotex Direct mRNA kit (Qiagen). mRNA was reverse transcribed into double stranded cDNA using a modified oligo18(dT) primer with an identifying tag sequence (see table below). cDNAs from different stages were pooled in equal amounts before adaptor ligation. Tag identification when sequencing from 5' end: Stage 1 (bud) insert 18(A)TCGGA; Stage 2 (balloon) insert 18(A)TCGGA; Stage 3 (open) insert 18(A)TCGCT; Stage 4 (after pollination) insert 18(A)TCGCT. Tag identification when sequencing from 3' end: Stage 1 (bud) TCCGATG insert; Stage 2 (balloon) TCCGATG insert; Stage 3 (open) ACCGATG insert; Stage 4 (after pollination) ACCGATG insert. Double stranded cDNAs were size selected (more than 450 bp), adaptor with EcoRI adapters at both ends and then digested with NotI. The cDNAs were then directionally cloned into EcoRI-NotI digested pBS II SK(+) phagemid vector (Stratagene). Identification of adaptors and tags in 5'-end sequenced clones: <vector>...TAAGCTT<End Vector><Start EcoRI adaptor>GATTCGAATTCGATGTTGCG<End EcoRI adaptor><Start insert>...AAAAAAAAAAAAAAAA<End insert><Start Tag>TCGCA<End Tag><Start NotI site/Vector>GCGCGCGCCACCGCGG... The total number of white colony forming units (cfu) in the primary library before amplification was 1.1x10<sup>6</sup> cfu (colony forming units). The background of empty clones was less than 1%. Inserts ranged from 0.5kb to 3 kb, as determined by PCR. Purified plasmid DNA from the primary library was converted to single-stranded circles and used as a template for PCR amplification using the T7 and T3 priming sites flanking the cloned cDNA inserts. The purified PCR products, representing the entire cloned cDNA population, were used as a driver for normalization. Hybridization between the single-stranded library and the PCR products was carried out for 44 hours at 30C. Unhybridized single-stranded DNA circles were separated from hybridized DNA rendered partially double-stranded and electroporated into DH10B cells to generate the normalized library. The total number of clones with insert was 9x10<sup>6</sup> cfu. Background of empty clones was less than 1%

ORIGIN

Query Match 1.5%; Score 29; DB 7; Length 472;  
Best Local Similarity 100.0%; Pred. No. 0.0035;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1555 GAGATGGCTCGCATGTTGCTTGCTGC 1583  
351 GAGATGGCTCGCATGTTGCTTGCTGC 379

RESULT 15  
LOCUS BM061076 505 bp mRNA linear EST 11-SEP-2002  
DEFINITION KS01026B11 KS01 Capsicum annuum cDNA, mRNA sequence.  
ACCESSION BM061076  
VERSION BM061076.1 GI:22781194  
KEYWORDS  
SOURCE  
ORGANISM Capsicum annuum

REFERENCE  
AUTHORS  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanales; Solanales; Capsicum.  
1 (bases 1 to 505)  
Lee, S.-Y., Chung, Y.-H., Shin, H.-J., Goh, S.-H., Pai, H.-S., Hur, C.-G., and Choi, D.  
Generation of Expressed Sequence Tags from Hot Pepper (Capsicum annuum L.) and Sequence Analysis in Relation to Hypersensitive Response Against Pathogen  
Unpublished (2001)  
Contact: Doll Choi  
Genome Research Center and National Center for Genome Information  
Korea Research Institute of Bioscience and Biotechnology

TITLE  
JOURNAL  
COMMENT

twice from total RNA from each stage using the Oligotex Direct mRNA kit (Qiagen). mRNA was reverse transcribed into double stranded cDNA using a modified oligo18(dT) primer with an identifying tag sequence (see table below). cDNAs from different stages were pooled in equal amounts before adaptor ligation. Tag identification when sequencing from 5' end: Stage 1 (bud) insert 18(A)TCGGA; Stage 2 (balloon) insert 18(A)TCGGA; Stage 3 (open) insert 18(A)TCGCT; Stage 4 (after pollination) insert 18(A)TCGCT. Tag identification when sequencing from 3' end: Stage 1 (bud) TCCGATG insert; Stage 2 (balloon) TCCGATG insert; Stage 3 (open) ACCGATG insert; Stage 4 (after pollination) ACCGATG insert. Double stranded cDNAs were size selected (more than 450 bp), adaptor with EcoRI adapters at both ends and then digested with NotI. The cDNAs were then directionally cloned into EcoRI-NotI digested pBS II SK(+) phagemid vector (Stratagene). Identification of adaptors and tags in 5'-end sequenced clones: <vector>...TAAGCTT<End Vector><Start EcoRI adaptor>GATTCGAATTCGATGTTGCG<End EcoRI adaptor><Start insert>...AAAAAAAAAAAAAAAA<End insert><Start Tag>TCGCA<End Tag><Start NotI site/Vector>GCGCGCGCCACCGCGG... The total number of white colony forming units (cfu) in the primary library before amplification was 1.1x10<sup>6</sup> cfu (colony forming units). The background of empty clones was less than 1%. Inserts ranged from 0.5kb to 3 kb, as determined by PCR. Purified plasmid DNA from the primary library was converted to single-stranded circles and used as a template for PCR amplification using the T7 and T3 priming sites flanking the cloned cDNA inserts. The purified PCR products, representing the entire cloned cDNA population, were used as a driver for normalization. Hybridization between the single-stranded library and the PCR products was carried out for 44 hours at 30C. Unhybridized single-stranded DNA circles were separated from hybridized DNA rendered partially double-stranded and electroporated into DH10B cells to generate the normalized library. The total number of clones with insert was 9x10<sup>6</sup> cfu. Background of empty clones was less than 1%

P.O. Box 115, Yuseong, Taejeon, 305-600, Republic of Korea

Tel: 82-42-860-4340

Fax: 82-42-860-4309

Email: doil@mail.kribd.re.kr

High quality sequence stop: 505.

Location/Qualifiers

1. .505

/organism="Capsicum annuum"

/mol\_type="mRNA"

/cultivar="Bukang"

/db\_xref="taxon:4072"

/tissue\_type="leaf"

/dev\_stage="8 weeks after germination"

/clone\_lib="KS01"

/note="Vector: pBluescript SK(-)"

# ORIGIN

Query Match 1.5%; Score 29; DB 4; length 505;

Best Local Similarity 100.0%; Pred.No. 0.0036;

Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1244 TTGCTGATTTTGGCTTTGCTTAAGATTGCT 1272

DB 58 TTGCTGATTTTGGCTTTGCTTAAGATTGCT 86

Search completed: November 13, 2004, 15:31:16  
Job time : 4240 secs